GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 87.8313 Seconds
(without alignments)
46.851 Million cell updates/sec

Title: US-10-062-257A-1
Perfect score: 45
Sequence: 1 TFDYLRSVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	4	AAG68079	Aag68079 Antitumou
2	45	100.0	9	4	AAB73117	Aab73117 Tumour an
3	45	100.0	9	6	ABR84376	Abr84376 Human lck
4	45	100.0	9	8	ADS87117	Ads87117 Human gen
5	45	100.0	9	9	ADX58317	Adx58317 Partial a
6	45	100.0	9	9	ADZ42232	Adz42232 Cytotoxic
7	45	100.0	9	9	AEC33132	Aec33132 Lck tumor
8	45	100.0	13	4	AAB73144	Aab73144 Tumour an
9	45	100.0	246	4	ABG22263	Abg22263 Novel hum
10	45	100.0	259	2	AAY43956	Aay43956 Mouse pro
11	45	100.0	259	2	AAY43955	Aay43955 Human pro
12	45	100.0	263	8	ADR88385	Adr88385 LCK tyros
13	45	100.0	265	7	ABR56203	Abr56203 Mutant Ly
14	45	100.0	271	7	ABR56204	Abr56204 Mutant Ly
15	45	100.0	279	9	ADY85449	Ady85449 Catalytic
16	45	100.0	346	3	AAY76750	Aay76750 Human pro
17	45	100.0	346	4	AAE06208	Aae06208 Human pro
18	45	100.0	346	5	ABB84435	Abb84435 Human pro
19	45	100.0	355	8	ABM82980	Abm82980 Human dia
20	45	100.0	417	2	AAR14201	Aar14201 (Beta-gal
21	45	100.0	458	7	ADC99048	Adc99048 Human KPP
22	45	100.0	502	5	AAE21689	Aae21689 Fugu rubr
23	45	100.0	508	3	AAB37700	Aab37700 Human lym
24	45	100.0	508	7	ADE58802	Ade58802 Human Pro
25	45	100.0	508	7	ADE58799	Ade58799 Human Pro
26	45	100.0	508	7	ADF45072	Adf45072 Human kin
27	45	100.0	508	7	ADL34479	Adl34479 Human lym
28	45	100.0	508	8	ADS88148	Ads88148 Human pro
29	45	100.0	509	3	AAY49420	Aay49420 PKA subst
30	45	100.0	509	6	ABR58699	Abr58699 Human can
31	45	100.0	509	7	ABR56202	Abr56202 Human Lym
32	45	100.0	509	7	ADE40449	Ade40449 Human pro
33	45	100.0	509	8	ADL22907	Adl22907 Human MP2
34	45	100.0	509	8	ADP12458	Adp12458 Protein e
35	45	100.0	509	8	ADP48374	Adp48374 Human lym
36	45	100.0	509	9	ADZ51107	Adz51107 Amino aci
37	45	100.0	509	9	AEA35921	Aea35921 Human Lck
38	45	100.0	539	8	ABM82981	Abm82981 Human dia
39	45	100.0	539	8	ABM82982	Abm82982 Human dia
40	45	100.0	551	4	ABG22264	Abg22264 Novel hum
41	45	100.0	567	5	ABG79673	Abg79673 Tumour in
42	41	91.1	9	4	AAB73123	Aab73123 Tumour an
43	41	91.1	13	4	AAB73149	Aab73149 Tumour an
44	41	91.1	251	9	ADY52569	Ady52569 Human onc
45	41	91.1	260	2	AAY43954	Aay43954 Human pro
46	41	91.1	439	9	ADY52636	Ady52636 Human tra
47	41	91.1	440	9	ADY52635	Ady52635 Human tra
48	41	91.1	444	9	ADY52634	Ady52634 Human tra
49	41	91.1	447	9	ADY52633	Ady52633 Human tra
50	41	91.1	452	9	ADY52632	Ady52632 Human tra
51	41	91.1	459	9	ADY52631	Ady52631 Human tra
52	41	91.1	467	9	ADY52630	Ady52630 Human tra
53	41	91.1	472	9	ADY52629	Ady52629 Human tra
54	41	91.1	473	9	ADY52628	Ady52628 Human tra
55	41	91.1	481	9	ADY52627	Ady52627 Human tra
56	41	91.1	483	9	ADY52626	Ady52626 Human tra
57	41	91.1	493	9	ADY52625	Ady52625 Human tra
58	41	91.1	511	7	ADF45073	Adf45073 Human kin
59	41	91.1	512	7	ADD19014	Add19014 Human dis
60	41	91.1	512	7	ADN95430	Adn95430 Human BEC
61	41	91.1	512	8	ADL22908	Adl22908 Human MP2
62	41	91.1	512	8	ADN04498	Adn04498 Antipsori
63	41	91.1	512	8	ADP12483	Adp12483 Protein e
64	41	91.1	512	8	ADR14269	Adr14269 Human NF-
65	41	91.1	512	8	ADS88430	Ads88430 Human pro
66	41	91.1	512	8	ADP23372	Adp23372 PRO polyp
67	41	91.1	512	9	ADY16487	Ady16487 PRO polyp
68	41	91.1	512	9	ADY19685	Ady19685 PRO polyp
69	41	91.1	512	9	ADY14848	Ady14848 PRO polyp
70	41	91.1	512	9	ADY52574	Ady52574 Human onc
71	41	91.1	512	9	AEA35920	Aea35920 Human Lyn
72	37	82.2	458	8	ADH22508	Adh22508 Human tra
73	37	82.2	559	8	ABM84024	Abm84024 Human dia
74	37	82.2	561	8	ADU24099	Adu24099 Human asp
75	37	82.2	606	5	ABP52121	Abp52121 Homo sapi
76	37	82.2	620	7	ADE10036	Ade10036 Novel pro
77	37	82.2	789	2	AAW14055	Aaw14055 Pumpkin e
78	37	82.2	789	8	ADM98975	Adm98975 Diterpene
79	37	82.2	822	7	ADE08716	Ade08716 Novel pro
80	36	80.0	260	2	AAY29671	Aay29671 Human src
81	36	80.0	260	4	AAU08733	Aau08733 Src-famil
82	36	80.0	308	6	ABU27400	Abu27400 Protein e
83	36	80.0	319	2	AAY37655	Aay37655 Amino aci
84	36	80.0	496	2	AAY29668	Aay29668 Human src
85	36	80.0	496	4	AAU08734	Aau08734 Xenopus l
86	36	80.0	496	4	AAU08730	Aau08730 Xenopus l
87	36	80.0	496	4	AAU08735	Aau08735 Xenopus l
88	35	77.8	9	4	AAB73124	Aab73124 Tumour an
89	35	77.8	13	4	AAG68083	Aag68083 Antitumou
90	35	77.8	13	4	AAB73150	Aab73150 Tumour an
91	35	77.8	250	9	ADY52570	Ady52570 Human onc
92	35	77.8	259	2	AAY43957	Aay43957 Human pro
93	35	77.8	271	8	ADR88384	Adr88384 HCK tyros
94	35	77.8	272	5	ABB81188	Abb81188 Human KIT
95	35	77.8	300	9	ADY85468	Ady85468 Catalytic
96	35	77.8	316	9	ADY85448	Ady85448 Catalytic

97	35	77.8	383	7	ADJ68978	Adj68978 Human hea
98	35	77.8	436	8	ADN61468	Adn61468 Human KPP
99	35	77.8	438	9	ADY52642	Ady52642 Human tra
100	35	77.8	458	8	ADJ71657	Adj71657 Human NOV

ALIGNMENTS

RESULT 1
AAG68079
ID AAG68079 standard; peptide; 9 AA.
XX
AC AAG68079;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide lck 486-494.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFDYLRSVL 9
              |||||||||
Db          1 TFDYLRSVL 9
```

RESULT 2
AAB73117
ID AAB73117 standard; peptide; 9 AA.
XX
AC AAB73117;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #1.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 1; Page 66; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TFDYLRSVL 9
              |||||||||
Db          1 TFDYLRSVL 9
```

RESULT 3
ABR84376
ID ABR84376 standard; peptide; 9 AA.
XX
AC ABR84376;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human lck HLA-A24 epitope, SEQ ID NO:26.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.

```
XX
PT   A detection method of antigen specific T-cells, comprises the use of
PT   plural antigenic peptides, useful in semi-quantitative determination of
PT   cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS   Example 8; Page 10; 18pp; Japanese.
XX
CC   The invention relates to a method for the detection of antigen specific T
CC   -cells in a blood sample involving the use of a plurality of antigenic
CC   peptides. The method comprises sampling of peripheral blood monocytes;
CC   stimulation of the collected peripheral blood monocytes with antigens
CC   without direct use of antigen presenting cells; and detection of T-cells
CC   specific to the antigen in the stimulated monocytes. The method is
CC   particularly used for the detection of cancer as it can be used in semi-
CC   quantitative determination of cancer specific T-cells. It can also be
CC   used for cancer vaccine therapy for patients with cervical or prostate
CC   cancer. The method can additionally be used to monitor of cellular
CC   immunity and cancer immune therapy by detection of specific T-cell
CC   frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC   leukocyte antigen) peptides of human origin used in an example from the
CC   invention
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 45;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db          1 TFDYLRSVL 9


RESULT 4
ADS87117
ID   ADS87117 standard; peptide; 9 AA.
XX
AC   ADS87117;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human genetic vaccine/ubiquitin (Ub)/Lck-related epitope peptide 2.
XX
KW   vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
KW   Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
KW   lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
KW   colon; bladder; breast; oesophagus; kidney; brain; human; epitope; Lck.
XX
OS   Homo sapiens.
XX
PN   WO2004035085-A1.
XX
PD   29-APR-2004.
XX
PF   16-OCT-2003; 2003WO-JP013279.
XX
PR   17-OCT-2002; 2002JP-00302816.
XX
PA   (KYUS-) KYUSHU TLO CO LTD.
XX
PI   Himeno K,  Furue M,  Maehara Y;
XX
DR   WPI; 2004-357144/33.
XX
PT   Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
PT   or cytokine genes for prevention and treatment of cancer.
XX
PS   Disclosure; SEQ ID NO 133; 266pp; Japanese.
XX
CC   The invention relates to a novel genetic vaccine containing the ubiquitin
CC   gene together with a gene encoding an antigenic protein containing a T-
CC   cell target sequence. The vaccine of the invention may be useful for
CC   prevention and treatment of cancers including melanoma, sarcoma, lymphoma
CC   (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
CC   of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
CC   colon, bladder, breast, oesophagus, kidney or brain. The current sequence
CC   is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide
CC   of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 45;  DB 8;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db          1 TFDYLRSVL 9


RESULT 5
ADX58317
ID   ADX58317 standard; peptide; 9 AA.
XX
AC   ADX58317;
XX
DT   21-APR-2005  (first entry)
XX
DE   Partial antigenic peptide #3 derived from p56.
XX
KW   cytostatic; vaccine; hematopoietic tumor; p56; immunotherapy.
XX
OS   Unidentified.
XX
PN   WO2005011723-A1.
XX
PD   10-FEB-2005.
XX
PF   05-AUG-2004; 2004WO-JP011232.
XX
PR   05-AUG-2003; 2003JP-00287208.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K;
XX
DR   WPI; 2005-152358/16.
XX
PT   Prevention and/or therapeutic agent of hematopoietic tumor useful for
PT   preventing and/or treating hematopoietic tumor, has peptides having amino
PT   acid sequences of partial peptide of p56lck, SART-1, SART-2, SART-3, or
PT   ART-1 protein.
XX
PS   Claim 1; SEQ ID NO 3; 41pp; Japanese.
XX
CC   The specification describes a remedy for a hematopoietic tumor. The
CC   remedy comprises one or more peptides derived from p56 (lck), SART-1,
CC   SART-2, SART-3, or ART-1 proteins as an active ingredient. The peptides
CC   induce specific cytotoxic T cells. The remedy of thr invention is useful
CC   for preventing and treating hematopoietic tumors comprising human
CC   leukocyte antigen (HLA)-A24 molecules on its cell surface. It is also
CC   useful in immunotherapy of hematopoietic tumors, and for treating
CC   malignant tumors such as acute myelogenous leukemia, acute lymphoblastic
CC   leukemia, chronic lymphocytic leukemia, malignant lymphoma, multiple
CC   myeloma, etc. . The present sequence represents a partial peptide derived
CC   from p56, and is used in the remedy of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 45;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db          1 TFDYLRSVL 9
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```
RESULT 6
ADZ42232
ID   ADZ42232 standard; peptide; 9 AA.
XX
AC   ADZ42232;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Cytotoxic T-lymphocyte epitope peptide, Lck-486.
XX
KW   antibody; vaccine; immune stimulation; cytotoxic T-lymphocyte.
XX
OS   Synthetic.
XX
PN   JP2005099001-A.
XX
PD   14-APR-2005.
XX
PF   20-AUG-2004; 2004JP-00240269.
XX
PR   31-AUG-2003; 2003JP-00348853.
XX
PA   (ITOK/) ITO K.
PA   (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
XX
DR   WPI; 2005-310369/32.
XX
PT   Measuring anti-peptide antibody, by preparing supports immobilized with
PT   different peptides, pouring test substance comprising peptide recognizing
PT   antibody on supports, adding labeled secondary antibody, measuring amount
PT   of label.
XX
PS   Example 1; SEQ ID NO 8; 22pp; Japanese.
XX
CC   The invention relates to a novel method for measuring an anti-peptide
CC   antibody. The method involves preparing several supports immobilized with
CC   different kinds of peptides, pouring a test substance comprising a
CC   peptide recognizing antibody onto prepared supports for reacting a
CC   peptide with an antibody, combining the peptide recognizing antibody with
CC   a labeled secondary antibody, measuring the amount of coupled label and
CC   identifying the kind of support for measuring the anti-peptide antibody.
CC   The invention further comprises a method for selecting a peptide vaccine
CC   candidate. The method enables the measurement of anti-peptide antibodies
CC   from trace amounts of a sample, e.g. blood serum from patients, rapidly
CC   with high efficiency. The immune response specific to a peptide vaccine
CC   can be monitored efficiently. This sequence represents a cytotoxic T-
CC   lymphocyte (CTL) epitope peptide of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 45;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db          1 TFDYLRSVL 9


RESULT 7
AEC33132
ID   AEC33132 standard; peptide; 9 AA.
XX
AC   AEC33132;
XX
DT   17-NOV-2005  (first entry)
XX
DE   Lck tumor antigen peptide SEQ ID NO 7.
XX
KW   cytostatic; vaccine; gene therapy; epitope; immunogenicity; diagnosis;
KW   tumor-associated antigen; cancer; neoplasm; Lck.
XX
OS   Homo sapiens.
XX
PN   WO2005083074-A1.
XX
PD   09-SEP-2005.
XX
PF   01-MAR-2005; 2005WO-JP003399.
XX
PR   01-MAR-2004; 2004JP-00056865.
XX
PA   (UYKA-) UNIV KANAZAWA TECHNOLOGY LICENSING ORG.
XX
PI   Kaneko S,  Mizukoshi E,  Nakamoto Y,  Tsuji H;
XX
DR   WPI; 2005-619189/63.
XX
PT   Novel tumor antigen peptide derived from Cyp-B, SART, p53, alpha-
PT   fetoprotein and human telomerase reverse transcriptase, useful for
PT   preparing anti-tumor peptide vaccine.
XX
PS   Example 1; SEQ ID NO 7; 58pp; Japanese.
XX
CC   The invention describes a tumor antigen peptide (I) including Cyp-B,
CC   SART, p53, multidrug resistance protein (MRP), alpha-fetoprotein (AFP) or
CC   human telomerase reverse transcriptase (hTERT) derived peptide comprising
CC   an amino acid sequence (S1) of SEQ ID No. 4, 14, 15, 18, 19, 23-25, 27-
CC   30, 34, 37-41 or 44. Also described are: an anti-tumor peptide vaccine
CC   comprising (I); antigen presenting cells (II) presenting (I), obtained by
CC   cultivating human leukocyte antigen (HLA)-A24 positive antigen presenting
CC   cells with (I); nucleic acid molecule (III) comprising a base sequence
CC   encoding (S1); an antibody (A1) capable of specifically binding to (I);
CC   inducing (M1) cytotoxic T cells, involves cultivating tumor tissue
CC   infiltrated lymphocyte or peripheral blood lymphocyte isolated from the
CC   HLA-A24 positive patient, with (I) and interleukin (IL)-2; and anti-tumor
CC   agent comprising (III) or the cytotoxic T cell acquired by (M1). (I) is
CC   useful for preparing anti-tumor peptide vaccine. The nucleic acid
CC   molecule is useful as an anti-tumor agent. The antibody is useful for
CC   detecting or diagnosing cancer. (I) is an effective immunogenic peptide
CC   with respect to tumor. This is the amino acid sequence of a Lck tumor
CC   antigen peptide. Note: This sequence is also available in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 45;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db          1 TFDYLRSVL 9


RESULT 8
AAB73144
ID   AAB73144 standard; peptide; 13 AA.
XX
AC   AAB73144;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Tumour antigen peptide #28.
XX
KW   Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS   Homo sapiens.
XX
PN   WO200111044-A1.
XX
PD   15-FEB-2001.
XX
PF   03-AUG-2000; 2000WO-JP005220.
```

XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Example 6; Page 36; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 45; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 1 TFDYLRSVL 9

RESULT 9
ABG22263
ID ABG22263 standard; protein; 246 AA.
XX
AC ABG22263;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22254.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86450.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 52622; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 45; DB 4; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 223 TFDYLRSVL 231

RESULT 10
AAY43956
ID AAY43956 standard; protein; 259 AA.
XX
AC AAY43956;
XX
DT 21-DEC-1999 (first entry)
XX
DE Mouse protein kinase #6.
XX
KW Prediction; secondary structure; alignment; evolutionary conservation;
KW homology; periodicity; co-variation analysis; antigenic site;
KW site directed mutagenesis; interaction.
XX
OS Mus sp.
XX
PN US5958784-A.
XX
PD 28-SEP-1999.
XX
PF 25-MAR-1992; 92US-00857224.
XX
PR 25-MAR-1992; 92US-00857224.
XX
PA (BENN/) BENNER S A.
XX
PI Benner SA;
XX
DR WPI; 1999-570766/48.
XX
PT Predicting the folded structure of proteins.
XX
PS Disclosure; Col 255-258; 113pp; English.
XX
CC Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC predicting the folded structure of proteins, by aligning sequences of
CC homologous proteins and using patterns of evolutionarily conserved and
CC varied sequences to assign positions. Positions in the alignment are
CC assigned to the surface or inside of the folded structure, active sites,
CC and parsing segments. Secondary structural units are assigned by
CC identifying periodicity in the assignments, and assembled into globular
CC form using distance constraints imposed by disulfide bridges, active site
CC assignments and co-variation analysis. The predicted secondary structures
CC are useful for identifying antigenic sites on a protein molecule, as
CC guides for site directed mutagenesis studies, and for understanding the

```
CC   interaction of a protein with other molecules
XX
SQ   Sequence 259 AA;

  Query Match            100.0%;  Score 45;  DB 2;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 0.91;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        244 TFDYLRSVL 252


RESULT 11
AAY43955
ID   AAY43955 standard; protein; 259 AA.
XX
AC   AAY43955;
XX
DT   21-DEC-1999  (first entry)
XX
DE   Human protein kinase #15.
XX
KW   Prediction; secondary structure; alignment; evolutionary conservation;
KW   homology; periodicity; co-variation analysis; antigenic site;
KW   site directed mutagenesis; interaction.
XX
OS   Homo sapiens.
XX
PN   US5958784-A.
XX
PD   28-SEP-1999.
XX
PF   25-MAR-1992;   92US-00857224.
XX
PR   25-MAR-1992;   92US-00857224.
XX
PA   (BENN/) BENNER S A.
XX
PI   Benner SA;
XX
DR   WPI; 1999-570766/48.
XX
PT   Predicting the folded structure of proteins.
XX
PS   Disclosure; Col 253-256; 113pp; English.
XX
CC   Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC   predicting the folded structure of proteins, by aligning sequences of
CC   homologous proteins and using patterns of evolutionarily conserved and
CC   varied sequences to assign positions. Positions in the alignment are
CC   assigned to the surface or inside of the folded structure, active sites,
CC   and parsing segments. Secondary structural units are assigned by
CC   identifying periodicity in the assignments, and assembled into globular
CC   form using distance constraints imposed by disulfide bridges, active site
CC   assignments and co-variation analysis. The predicted secondary structures
CC   are useful for identifying antigenic sites on a protein molecule, as
CC   guides for site directed mutagenesis studies, and for understanding the
CC   interaction of a protein with other molecules
XX
SQ   Sequence 259 AA;

  Query Match            100.0%;  Score 45;  DB 2;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 0.91;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        244 TFDYLRSVL 252


RESULT 12
ADR88385
ID   ADR88385 standard; protein; 263 AA.
XX
AC   ADR88385;
XX
DT   18-NOV-2004  (first entry)
XX
DE   LCK tyrosine kinase protein.
XX
KW   Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW   G-protein coupled receptor; methyl transferase; ligase;
KW   LCK tyrosine kinase; enzyme.
XX
OS   Unidentified.
XX
PN   US2004171062-A1.
XX
PD   02-SEP-2004.
XX
PF   28-FEB-2003; 2003US-00377268.
XX
PR   28-FEB-2002; 2002US-0360651P.
PR   16-SEP-2002; 2002US-0411398P.
PR   20-SEP-2002; 2002US-0412341P.
PR   02-JAN-2003; 2003US-0437929P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Hirth K,  Milburn MV;
XX
DR   WPI; 2004-642017/62.
XX
PT   Designing a ligand binding to a target molecule, comprises identifying as
PT   molecular scaffolds compounds binding to members of a molecular family,
PT   detecting orientation of scaffolds at a binding site of target, and
PT   synthesizing ligand.
XX
PS   Disclosure; SEQ ID NO 24; 186pp; English.
XX
CC   The present invention relates to a method of designing a ligand binding
CC   to a target molecule. The method involves identifying as molecular
CC   scaffolds compounds binding to members of a molecular family, detecting
CC   orientation of scaffolds at a binding site of target, and synthesising
CC   ligand. The invention is useful for designing drug products and for
CC   designing ligand binding to target molecules such as nuclear hormone
CC   receptors, TNF receptors, G-protein coupled receptors, methyl
CC   transferases, ligases, etc. The present sequence is the LCK tyrosine
CC   kinase protein. This sequence is used to illustrate the method of
CC   invention.
XX
SQ   Sequence 263 AA;

  Query Match            100.0%;  Score 45;  DB 8;  Length 263;
  Best Local Similarity   100.0%;  Pred. No. 0.93;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        248 TFDYLRSVL 256


RESULT 13
ABR56203
ID   ABR56203 standard; protein; 265 AA.
XX
AC   ABR56203;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).
XX
KW   Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW   Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW   mutant.
```

```
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 128
FT                   /note= "Wild-type D substituted with N. This position is
FT                   364 in the full-length sequence (see ABR56202 for the
FT                   wild-type full length sequence"
FT   Modified-site   158
FT                   /note= "Phosphorylation site"
XX
PN   WO2003020880-A2.
XX
PD   13-MAR-2003.
XX
PF   02-AUG-2002; 2002WO-US024546.
XX
PR   03-AUG-2001; 2001US-0310051P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Borhani DW,  Calderwood D,  Dixon RW,  Hirst GC,  Hrnciar P,  Loew A;
PI   Leung A,  Ritter K;
XX
DR   WPI; 2003-300872/29.
XX
PT   New crystalline polypeptide comprising ligand binding domain or catalytic
PT   domain of Lck protein, for determining three-dimensional structure of
PT   catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS   Claim 12; Fig 2; 994pp; English.
XX
CC   The present invention relates to a crystalline polypeptide (I),
CC   comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC   protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC   in T-cells and plays an essential role in immune response. (I) is useful
CC   for identifying a compound which is an inhibitor of human Lck protein.
CC   The present sequence is a mutated fragment of the human Lck sequence,
CC   which approximately comprises the catalytic domain
XX
SQ   Sequence 265 AA;

  Query Match             100.0%;  Score 45;  DB 7;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 0.93;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        250 TFDYLRSVL 258


RESULT 14
ABR56204
ID   ABR56204 standard; protein; 271 AA.
XX
AC   ABR56204;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N).
XX
KW   Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW   Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW   mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 134
FT                   /note= "Wild-type D substituted with N. This position is
FT                   364 in the full-length sequence (see ABR56202 for the
FT                   wild-type full length sequence"
FT   Modified-site   164
FT                   /note= "Phosphorylation site"
XX
PN   WO2003020880-A2.
XX
PD   13-MAR-2003.
XX
PF   02-AUG-2002; 2002WO-US024546.
XX
PR   03-AUG-2001; 2001US-0310051P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Borhani DW,  Calderwood D,  Dixon RW,  Hirst GC,  Hrnciar P,  Loew A;
PI   Leung A,  Ritter K;
XX
DR   WPI; 2003-300872/29.
XX
PT   New crystalline polypeptide comprising ligand binding domain or catalytic
PT   domain of Lck protein, for determining three-dimensional structure of
PT   catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS   Example 1; Fig 3; 994pp; English.
XX
CC   The present invention relates to a crystalline polypeptide (I),
CC   comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC   protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC   in T-cells and plays an essential role in immune response. (I) is useful
CC   for identifying a compound which is an inhibitor of human Lck protein.
CC   The present sequence is a mutated fragment of the human Lck sequence,
CC   which approximately comprises the catalytic domain
XX
SQ   Sequence 271 AA;

  Query Match             100.0%;  Score 45;  DB 7;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 0.96;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        256 TFDYLRSVL 264


RESULT 15
ADY85449
ID   ADY85449 standard; protein; 279 AA.
XX
AC   ADY85449;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Catalytic domain of PIM kinase-like protein LCK.
XX
KW   Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW   neoplasm; inflammation; antiinflammatory.
XX
OS   Unidentified.
XX
PN   WO2005028624-A2.
XX
PD   31-MAR-2005.
XX
PF   15-SEP-2004; 2004WO-US030360.
XX
PR   15-SEP-2003; 2003US-0503277P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Artis DR,  Bremer RE,  Gillette SJ,  Hurt CR,  Ibrahim PL;
PI   Zuckerman RL;
XX
DR   WPI; 2005-273155/28.
```

XX
PT New scaffold library used for identifying and developing ligands for
PT protein kinases and treating kinase associated disorders e.g. cancer,
PT comprises set of compounds comprising N-heterocyclic compounds.
XX
PS Disclosure; Page 170-174; 236pp; English.
XX
CC The invention relates to a new kinase scaffold library comprises at least
CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
CC compound of formulae (I)-(VII) given in the specification. Also included
CC are a system for fitting compounds in binding sites of protein kinases
CC (comprising an electronic kinase scaffold, and a scaffold library
CC comprising at least 1 collection of electronic representations of (I)-
CC (VII), where the scaffold library is embedded in a computer device and
CC the electronic representations of the compounds can be selectively
CC retrieved and functionally connected with computer software adapted to
CC fit electronic representations of compounds in an electronic
CC representation of a binding site of a kinase), obtaining improved ligands
CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the compound or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group, and developing a ligand for a kinase
CC comprising conserved residues matching at least on of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease
CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 45; DB 9; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 256 TFDYLRSVL 264

RESULT 16
AAY76750

ID AAY76750 standard; protein; 346 AA.
XX
AC AAY76750;
XX
DT 17-APR-2000 (first entry)
XX
DE Human protein kinase homologue, PKH-3.
XX
KW Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS;
KW autoimmune disorder; inflammatory disorder; reproductive defect; asthma;
KW diabetes mellitus; infertility; ovulatory defect; endometriosis;
KW polycystic ovary syndrome.
XX
OS Homo sapiens.
XX
PN US6013455-A.
XX
PD 11-JAN-2000.
XX
PF 15-OCT-1998; 98US-00173581.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Yue H, Yang YT, Corley NC, Gorgone GA, Azimzai Y;
PI Lu DAM, Bandman O, Guegler KJ;
XX
DR WPI; 2000-136321/12.
DR N-PSDB; AAZ86794.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX
PS Claim 1; Col 47-50; 38pp; English.
XX
CC This sequence represents a human protein kinase homolog (PKH) of the
CC invention. The PKH sequences may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate PKH expression such
CC as cancers, autoimmune/inflammatory disorders and reproductive defects.
CC They may be used to treat disorders associated with decreased PKH
CC expression such as cancers (e.g. lymphoma, melanoma and cancers of the
CC breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS,
CC asthma and diabetes mellitus), and reproductive defects (e.g.
CC infertility, ovulatory defects, endometriosis and polycystic ovary
CC syndrome). The DNA may be administered to treat diseases by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC PKH by expressing inactive proteins or to supplement the patients own
CC production of PKH polypeptides. Additionally, the DNA may be used to
CC produce PKH, according to standard recombinant DNA methodology, by
CC inserting the nucleic acids into a host cell and culturing the cell to
CC express the protein. Conversely, antisense nucleic acid molecules may be
CC administered to down regulate PKH expression by binding with the cells
CC own PKH genes and preventing their expression. The DNA, and antisense
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acid sequences in samples,
CC and hence which patients may be in need of restorative therapy. They may
CC also be used to study the expression and function of PKH polypeptides and
CC their role in metabolism. The PKH polypeptides may be used as antigens in
CC the production of antibodies against PKH and in assays to identify
CC modulators (agonists and antagonists) of PKH expression and activity. The
CC anti-PKH antibodies and PKH antagonists may also be used to down regulate
CC PKH expression and activity. The anti-PKH antibodies may also be used as
CC diagnostic agents for detecting the presence of PKH polypeptides in
CC samples
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 45; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TFDYLRSVL 9
              |||||||||
Db        323 TFDYLRSVL 331
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RESULT 17
AAE06208
ID AAE06208 standard; protein; 346 AA.
XX
AC AAE06208;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein kinase homolog-3 (PKH-3).
XX
KW Human; protein kinase homolog-3; PKH-3; cytostatic; protein therapy;
KW vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma;
KW Acquired Immune deficiency Syndrome; AIDS; melanoma; cancer; bone; liver;
KW breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia;
KW Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder;
KW reproductive disorder; polycystic ovary syndrome; asthma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 125. .333
FT /note= "Signature sequence"
XX
PN US6264947-B1.
XX
PD 24-JUL-2001.
XX
PF 20-OCT-1999; 99US-00420915.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2001-450728/48.
DR N-PSDB; AAD11845.
XX
PT Human protein kinase proteins and homologs, useful for preventing,
PT diagnosing and treating cancers, autoimmune/inflammatory disorders and
PT reproductive disorders.
XX
PS Claim 1; Col 47-50; 38pp; English.
XX
CC The present sequence is human protein kinase homolog-3 (PKH-3). Human
CC protein kinase homologs (PKH) and their cDNA molecules are used in the
CC prevention, diagnosis and treatment of diseases associated with increased
CC or decreased expression of PKH. Examples of such disorders include,
CC cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer),
CC autoimmune/inflammatory disorders (e.g. Acquired Immune deficiency
CC Syndrome (AIDS), anaemia, asthma, Crohn's disease and multiple sclerosis)
CC and reproductive disorders (e.g. tubal disease, ectopic pregnancy and
CC polycystic ovary syndrome). PKH, its catalytic or immunogenic fragment
CC are used for screening libraries of compounds in any of the drug
CC screening techniques. PKH nucleic acids are used to generate
CC hybridisation probes useful in mapping the naturally occurring genomic
CC sequences. PKH are also used as antigens in the production of antibodies
CC against protein kinases (PK) and in assays to identify modulators of PK
CC expression and activity. PKH is also used in protein therapy
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 45; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFDYLRSVL 9
              |||||||||
Db        323 TFDYLRSVL 331
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RESULT 18
ABB84435
ID ABB84435 standard; protein; 346 AA.
XX
AC ABB84435;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human protein kinase homologue from clone 507669.
XX
KW Protein kinase homologue; PKH; cytostatic; immunosuppressive; antifungal;
KW antiinflammatory; antiallergic; antiasthmatic; antianaemic; antidiabetic;
KW antiarteriosclerotic; antithyroid; dermatological; nephrotropic; human;
KW antigout; thyromimetic; nootropic; osteopathic; antiarthritic; allergy;
KW antirheumatic; ophthalmological; antiulcer; antiviral; antibacterial;
KW antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis;
KW acquired immunodeficiency syndrome; AIDS; Addison's disease; amyloidosis;
KW adult respiratory distress syndrome; anaemia; asthma; atherosclerosis;
KW autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis;
KW cholecystitis; contact dermatitis; Crohn's disease; atopic dermatitis;
KW dermatomyositis; diabetes mellitus; emphysema; atrophic gastritis; gout;
KW glomerulonephritis; Goodpasture's syndrome; Graves' disease; psoriasis;
KW Hashimoto's thyroiditis; hypereosinophilia; irritable bowel syndrome;
KW multiple sclerosis; myasthenia gravis; myocardial inflammation; uveitis;
KW pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis;
KW polymyositis; Reiter's syndrome; rheumatoid arthritis; scleroderma; SLE;
KW Sjogren's syndrome; systemic lupus erythematosus; systemic sclerosis;
KW thrombocytopenic purpura; ulcerative colitis; Werner syndrome; infection;
KW haemodialysis; extracorporeal circulation; infertility; tubal disease;
KW ovulatory defect; endometriosis; oestrous; menstrual cycle; gene therapy;
KW uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme;
KW ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis;
KW cancer.
XX
OS Homo sapiens.
XX
PN US2002081290-A1.
XX
PD 27-JUN-2002.
XX
PF 30-MAY-2001; 2001US-00870962.
XX
PR 15-OCT-1998; 98US-00173581.
PR 20-OCT-1999; 99US-00420915.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2002-655433/70.
DR N-PSDB; ABQ76288.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX
PS Claim 47; Page 27; 43pp; English.
XX
CC This invention describes a novel protein kinase homologue (PKH)
CC polypeptides which have cytostatic, immunosuppressive, antiinflammatory,
CC antiallergic, antiasthmatic, antianaemic, antiarteriosclerotic,
CC antithyroid, dermatological, antidiabetic, nephrotropic, antigout,
CC thyromimetic, nootropic, osteopathic, antiarthritic, antirheumatic,
CC ophthalmological, antiulcer, antiviral, antibacterial, antifungal,
CC antiprotozoal, antiparasitic and antihelmintic activity. The polypeptide
CC is used for treating a disease or condition associated with decreased
CC expression of functional PKH. The polypeptide is used to screen for
CC agonists and antagonists of PKH which can also be used in disease

```
CC   treatment. The polypeptide and polynucleotide are used for treating
CC   acquired immunodeficiency syndrome (AIDS), Addison's disease, adult
CC   respiratory distress syndrome, allergies, ankylosing spondylitis,
CC   amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer,
CC   contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis,
CC   diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis,
CC   Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis,
CC   hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
CC   myasthenia gravis, myocardial or pericardial inflammation,
CC   osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC   Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC   systemic lupus erythematosus (SLE), systemic sclerosis, thrombocytopenic
CC   purpura, ulcerative colitis, uveitis, Werner syndrome, complications of
CC   cancer, haemodialysis, and extracorporeal circulation, viral, bacterial,
CC   fungal, parasitic, protozoal, and helminthic infections, infertility,
CC   including tubal disease, ovulatory defects, and endometriosis,
CC   disruptions of the oestrous cycle, disruptions of the menstrual cycle,
CC   polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial
CC   and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic
CC   pregnancies, and teratogenesis. The polypeptides of the invention can be
CC   used for gene therapy. This sequence represents a PKH from clone ID
CC   507669 isolated from TMLR3DT02, a library constructed using RNA isolated
CC   from non-adherent peripheral blood mononuclear cells collected from a
CC   pool of male and female donors
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 45;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        323 TFDYLRSVL 331


RESULT 19
ABM82980
ID   ABM82980 standard; protein; 355 AA.
XX
AC   ABM82980;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3229.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN41632.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 355 AA;

  Query Match             100.0%;  Score 45;  DB 8;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        332 TFDYLRSVL 340


RESULT 20
AAR14201
ID   AAR14201 standard; protein; 417 AA.
XX
AC   AAR14201;
XX
DT   13-DEC-1991  (first entry)
XX
DE   (Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
XX
KW   Multi-cloning site.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .26
FT                   /note= "beta-galactosidase fragment"
FT   Region          27. .417
FT                   /note= "lck gene polypeptide"
XX
PN   JP03201994-A.
XX
PD   03-SEP-1991.
XX
PF   28-DEC-1989;   89JP-00338268.
XX
PR   28-DEC-1989;   89JP-00338268.
XX
PA   (TOKU ) TOKUYAMA SODA KK.
XX
DR   WPI; 1991-300980/41.
DR   N-PSDB; AAQ14201.
XX
PT   Fused polypeptide - has amino acid sequence of beta-galactosidase with a
PT   LCK gene conjugated to the N-terminal via DNA having multi-cloning site.
XX
PS   Claim 1; Fig 4,2; 15pp; Japanese.
```

XX
CC The sequence consists of the N-terminal amino acids of the beta-
CC galactosidase gene fused with the lck gene. It is produced by E.coli
CC transformed with a recombinant vector (see AAQ13983). It is useful for
CC producing an antibody specifically immunoreactive with only a lck gene-
CC derived polypeptide in T cells. The antibody may recognise lck gene-
CC derived polypeptides in human cells
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 45; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 394 TFDYLRSVL 402

RESULT 21
ADC99048
ID ADC99048 standard; protein; 458 AA.
XX
AC ADC99048;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human KPP protein - SEQ ID 1.
XX
KW anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
KW cancer; developmental; mental retardation; neurological;
KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; human; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003033680-A2.
XX
PD 24-APR-2003.
XX
PF 17-OCT-2002; 2002WO-US033723.
XX
PR 19-OCT-2001; 2001US-0345474P.
PR 02-NOV-2001; 2001US-0343910P.
PR 13-NOV-2001; 2001US-0333098P.
PR 16-NOV-2001; 2001US-0332424P.
PR 30-NOV-2001; 2001US-0334288P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
PI Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
PI Zebarjadian Y;
XX
DR WPI; 2003-403214/38.
DR N-PSDB; ADC99100.
XX
PT New human kinases and phosphatases and polynucleotides, useful for
PT diagnosing, treating or preventing autoimmune or inflammatory disorders
PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT cancer or hepatitis.
XX
PS Claim 1; SEQ ID NO 1; 424pp; English.
XX
CC The invention relates to a novel isolated polypeptide which is a human
CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
CC agonists and antagonists are useful for diagnosing, treating or
CC preventing cell proliferative disorders such as atherosclerosis,
CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
CC retardation, neurological disorders including Alzheimer's disease and
CC Parkinson's disease, autoimmune and inflammatory disorders such as
CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,
CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the
CC polynucleotides encoding KPP may be useful for creating transgenic
CC animals to model human disease, as well as during gene therapy
CC procedures. The current sequence is that of the human KPP protein of the
CC invention.
XX
SQ Sequence 458 AA;

Query Match 100.0%; Score 45; DB 7; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 435 TFDYLRSVL 443

RESULT 22
AAE21689
ID AAE21689 standard; protein; 502 AA.
XX
AC AAE21689;
XX
DT 29-AUG-2003 (revised)
DT 16-JUL-2002 (first entry)
XX
DE Fugu rubripes lymphocyte kinase (LCK) protein.
XX
KW T-lymphocyte modulator; autoimmune disorder; graft rejection;
KW graft-versus-host disease; viral infection; lymphocyte kinase; LCK.
XX
OS Takifugu rubripes.
XX
PN WO200218619-A2.
XX
PD 07-MAR-2002.
XX
PF 16-AUG-2001; 2001WO-IL000765.
XX
PR 01-SEP-2000; 2000US-0229326P.
XX
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA (EHRL/) EHRLICH G.
XX
PI Brenner S, Venkatesh B, Tan YH;
XX
DR WPI; 2002-329781/36.
DR N-PSDB; AAD34173.
XX
PT New nucleic acids, useful for regulating T-cell mediated immune
PT responses, e.g., suppressing T-lymphocytes in subjects with autoimmune
PT disorders, or enhancement in those with viral infections, comprises novel
PT T-cell active promoters.
XX
PS Example 2; Page 55-57; 67pp; English.
XX
CC The invention relates to an isolated nucleic acid which includes a
CC promoter sequence being transcriptionally functional in a T-lymphocyte
CC undergoing activation and transcriptionally less functional in the T-
CC lymphocyte prior to the activation. The nucleic acid is useful for
CC regulating T-cell mediated immune responses in mammals. Nucleic acid
CC molecules of the invention may be used to suppress or eliminate T-

```
CC   lymphocytes undergoing activation to suppress T-lymphocyte mediated
CC   immune response in individuals suffering from immune disorders, e.g.
CC   autoimmune disorders such as graft rejection or graft-versus-host
CC   disease. They may also be used to enhance T-lymphocyte mediated immune
CC   response in individual suffering from, e.g. viral infection. The present
CC   sequence is Fugu rubripes lymphocyte kinase (LCK) protein. (Updated on 29
CC   -AUG-2003 to standardise OS field)
XX
SQ   Sequence 502 AA;

  Query Match             100.0%;  Score 45;  DB 5;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        481 TFDYLRSVL 489


RESULT 23
AAB37700
ID   AAB37700 standard; protein; 508 AA.
XX
AC   AAB37700;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human lymphocyte kinase.
XX
KW   Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
XX
OS   Homo sapiens.
XX
PN   WO200070030-A1.
XX
PD   23-NOV-2000.
XX
PF   19-MAY-2000; 2000WO-US013881.
XX
PR   19-MAY-1999;   99US-0134965P.
XX
PA   (KINE-) KINETIX PHARM INC.
XX
PI   Zhu X;
XX
DR   WPI; 2000-687708/67.
XX
PT   Crystal of a protein-ligand complex for identifying kinase inhibitors,
PT   comprises a truncated lymphocyte kinase and a ligand, and diffracts X-
PT   rays to determine atomic coordinates at a resolution greater than 5
PT   angstroms.
XX
PS   Claim 1; Page 434-5; 438pp; English.
XX
CC   The present invention relates to a crystal of a protein-ligand complex
CC   comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal
CC   diffracts X-rays so that the atomic coordinates of the protein-ligand
CC   complex can be determined to a resolution of greater than 5.0 Angstroms.
CC   The truncated lck used in the present invention comprises the globular
CC   core of the corresponding full-length lck. The present sequence is the
CC   full-length human lck protein. The crystal of the present invention may
CC   be used to identify kinase inhibitors in screening assays, in drug
CC   screening and drug design processes, to design, select or test inhibitors
CC   of kinase enzymes, where the inhibitors are used as therapeutics for the
CC   treatment and modulation of diseases, disease symptoms or the effect of
CC   other physiological events mediated by kinases, having one or more kinase
CC   enzymes involved in their pathology
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 45;  DB 3;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        485 TFDYLRSVL 493


RESULT 24
ADE58802
ID   ADE58802 standard; protein; 508 AA.
XX
AC   ADE58802;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06239, SEQ ID NO 4689.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
```

SQ Sequence 508 AA;

Query Match 100.0%; Score 45; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 485 TFDYLRSVL 493

RESULT 25
ADE58799
ID ADE58799 standard; protein; 508 AA.
XX
AC ADE58799;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P06239, SEQ ID NO 4686.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P06239.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 45; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 485 TFDYLRSVL 493

RESULT 26
ADF45072
ID ADF45072 standard; protein; 508 AA.
XX
AC ADF45072;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human kinase LCK.
XX
KW Human; protein kinase; enzyme; inhibitor; LCK.
XX
OS Homo sapiens.
XX
PN WO2003081210-A2.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-US008725.
XX
PR 21-MAR-2002; 2002US-0366892P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Prescott JC, Braisted A;
XX
DR WPI; 2003-865136/80.
XX
PT Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.
XX
PS Disclosure; SEQ ID NO 41; 260pp; English.
XX
CC The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T)..The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 45; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 485 TFDYLRSVL 493

RESULT 27
ADL34479
ID ADL34479 standard; peptide; 508 AA.
XX
AC ADL34479;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human lymphocyte kinase (Lck) globular core.
XX
KW cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;
KW fungicide; nootropic; neuroprotective; kinase inhibitor; crystal;
KW protein-ligand complex; lymphocyte kinase; Lck; Lck ligand;
KW kinase inhibitor; therapeutic; kinase-mediated physiological event;
KW cancer; autoimmunological; metabolic; inflammatory; infection;
KW central nervous system degenerative disease; transplant rejection; human;
KW globular core; protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN US6589758-B1.
XX
PD 08-JUL-2003.
XX
PF 21-MAY-2001; 2001US-00862154.
XX
PR 19-MAY-2000; 2000US-0205510P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zhu X;
XX
DR WPI; 2003-810380/76.
XX
PT Crystal of protein-ligand complex useful for identifying an inhibitor of
PT lymphocyte kinase (Lck), comprises truncated Lck and a ligand.
XX
PS Claim 1; SEQ ID NO 1; 295pp; English.
XX
CC The invention describes a crystal (I) of a protein-ligand complex (C)
CC comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I)
CC effectively diffracts X-rays for determination of atomic coordinates of
CC (C) to a resolution of greater than 5.0 angstroms, and truncated Lck
CC comprises a sequence (S1) of residues 225-508 of a 508 amino acid
CC sequence, given in specification and retains the globular core of full-
CC length Lck. (I) is useful in an inhibitor screening assay and to
CC identify, design, select, and evaluate potential inhibitors of kinases
CC that would be useful as therapeutics for diseases or symptoms of diseases
CC that are associated with kinase-mediated physiological events. The
CC inhibitors identified by the methods may also be useful for inhibition of
CC kinase activity of one or more enzymes. The inhibitors are also useful
CC for inhibiting the biological activity of any enzyme comprising greater
CC than 90%, alternatively greater than 85%, or alternatively greater than
CC 70% sequence homology with a kinase sequence. The inhibitors are useful
CC for inhibiting the biological activity of any enzyme that binds ATP and
CC thus for treating disease or disease symptoms mediated by any enzyme that
CC binds ATP. The inhibitors are useful in inhibiting kinase activity and
CC are useful in treating kinase-mediated disease or disease symptoms in a
CC mammal, particularly a human e.g., cancer, autoimmunological, metabolic,
CC inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central
CC nervous system degenerative disease etc. The inhibitors are useful in
CC treating or preventing diseases, including, transplant rejection etc.
CC This is the amino acid sequence of a human lymphocyte kinase (Lck)
CC polypeptide comprising the Lck globular core.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 45; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 485 TFDYLRSVL 493

RESULT 28
ADS88148
ID ADS88148 standard; protein; 508 AA.
XX
AC ADS88148;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
XX
KW protein complex; tumour necrosis factor-alpha signalling pathway;
KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004035783-A2.
XX
PD 29-APR-2004.
XX
PF 24-SEP-2003; 2003WO-EP050655.
XX
PR 26-SEP-2002; 2002EP-00021809.
PR 10-FEB-2003; 2003EP-00100274.
XX
PA (CELL-) CELLZOME AG.
XX
PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI Superti-Furga G, Kruse U;
XX
DR WPI; 2004-348460/32.
XX
PT New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.
XX
PS Example; SEQ ID NO 3; 1980pp; English.
XX
CC This invention relates to novel protein complexes of the tumour necrosis
CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 45; DB 8; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||

```
Db        485 TFDYLRSVL 493


RESULT 29
AAY49420
ID   AAY49420 standard; protein; 509 AA.
XX
AC   AAY49420;
XX
DT   13-MAR-2000  (first entry)
XX
DE   PKA substrate, Src-family protein.
XX
KW   Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW   kinase substrate; immunosuppressive disorder; proliferative disease;
KW   HIV infection; AIDS; immunodeficiency; autoimmune disease;
KW   systemic lupus erythematosus; Src-family.
XX
OS   Homo sapiens.
XX
PN   WO9962315-A2.
XX
PD   02-DEC-1999.
XX
PF   27-MAY-1999;   99WO-GB001680.
XX
PR   27-MAY-1998;   98NO-00002419.
PR   30-DEC-1998;   98US-0114240P.
XX
PA   (LAUR-) LAURAS AS.
PA   (JONE/) JONES E L.
XX
PI   Hansson V,  Levy FO,  Mustelin T,  Skalhegg BS,  Sundvold V;
PI   Tasken K,  Vang T,  Altman A,  Munshi A;
XX
DR   WPI; 2000-086801/07.
DR   N-PSDB; AAZ46491.
XX
PT   Altering the activity of protein kinase signaling pathways, used for
PT   treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,
PT   e.g. cancers or autoimmune diseases.
XX
PS   Claim 23; Page 95-96; 111pp; English.
XX
CC   The invention provides a novel method of altering the activity of the
CC   protein kinase A (PKA) signaling pathway in a cell that comprises
CC   altering the extent of phosphorylation of one or more PKA substrates, or
CC   kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC   compositions containing a nucleic acid molecule that encodes a PKA
CC   substrate, or fragment, precursor or functionally equivalent variant,
CC   where the sequence is modified to alter its susceptibility to
CC   phosphorylation by PKA can be used for treating a disorder exhibiting
CC   abnormal PKA signaling activity, immunosuppressive disorders or
CC   proliferative diseases. They can be used for treating e.g. HIV infection,
CC   AIDS, common variable immunodeficiency or cancers. Conditions in which
CC   upregulation of the PKA pathway is required, such as autoimmune disease,
CC   e.g. systemic lupus erythematosus, may also be treated. The present
CC   sequence represents a PKA substrate, wherein the substrate is in the Src-
CC   family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl,
CC   Fyk, Src-1 or Src-2
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 45;  DB 3;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        486 TFDYLRSVL 494


RESULT 30
ABR58699
ID   ABR58699 standard; protein; 509 AA.
XX
AC   ABR58699;
XX
DT   09-JUL-2003  (first entry)
XX
DE   Human cancer related protein SEQ ID NO:356.
XX
KW   Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW   heart disease; atherosclerosis; endometriosis.
XX
OS   Homo sapiens.
XX
PN   WO2003025138-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-US029560.
XX
PR   17-SEP-2001; 2001US-0323469P.
PR   20-SEP-2001; 2001US-0323887P.
PR   13-NOV-2001; 2001US-0350666P.
PR   08-FEB-2002; 2002US-0355145P.
PR   08-FEB-2002; 2002US-0355257P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Gish KC,  Hevezi PA,  Mack DH,  Wilson KE;
PI   Zlotnik A;
XX
DR   WPI; 2003-354600/33.
DR   N-PSDB; ACC72850.
XX
PT   New genes that are up-regulated or down-regulated in cancers, useful as
PT   markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT   therapeutic targets for screening drugs for treating these diseases.
XX
PS   Claim 12; Page 762; 767pp; English.
XX
CC   The present invention describes an isolated nucleic acid molecule, which
CC   comprises the sequence of any of the genes that are up-regulated or down-
CC   regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC   acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC   related gene nucleotide sequences which encode the proteins given in
CC   ABR58521 to ABR58709. Also described: (1) determining the presence or
CC   absence of a pathological cell in a patient; (2) an expression vector
CC   comprising a nucleic acid molecule described above; (3) a host cell
CC   comprising the vector; (4) an isolated polypeptide, which is encoded by
CC   the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC   of (4); (6) specifically targeting a compound to a pathological cell in a
CC   patient by administering to the patient the antibody above; and (7) a
CC   drug screening assay. The nucleic acid is useful as diagnostic markers or
CC   therapeutic targets. In particular, the nucleic acid is useful for
CC   diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC   bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC   pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC   atherosclerosis and endometriosis. The nucleic acid is also useful in
CC   drug screening, particularly for identifying agents for treating these
CC   pathologies
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 45;  DB 6;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        486 TFDYLRSVL 494
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Search completed: June 29, 2006, 09:13:07
Job time : 88.8313 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on:: June 29, 2006, 09:13:45 ; Search time 13.3373 Seconds
(without alignments)
64.927 Million cell updates/sec

Title: US-10-062-257A-1
Perfect score: 45
Sequence: 1 TFDYLRSVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	509	1	I48845	protein-tyrosine k
2	45	100.0	509	1	OKHULK	protein-tyrosine k
3	41	91.1	512	1	A39719	protein-tyrosine k
4	41	91.1	512	1	I56160	protein-tyrosine k
5	41	91.1	512	1	TVHULY	protein-tyrosine k
6	37	82.2	379	2	AF2409	mannosyl transfera
7	37	82.2	509	1	TVHAST	protein-tyrosine k
8	37	82.2	606	2	JC5604	ABC-transporting p
9	37	82.2	789	2	T09672	ent-kaurene syntha
10	36	80.0	308	2	C81658	lipoic acid synthe
11	36	80.0	311	2	F71500	probable lipoate s
12	36	80.0	507	1	A39939	protein-tyrosine k
13	36	80.0	2708	2	T09079	probable chloroqui
14	36	80.0	2819	2	T09080	probable chloroqui
15	35	77.8	157	2	T27697	VPS29-like phospho
16	35	77.8	503	1	JQ1321	protein-tyrosine k
17	35	77.8	503	1	TVMSHC	protein-tyrosine k
18	35	77.8	505	1	TVHUHC	protein-tyrosine k
19	35	77.8	877	2	H71647	alanine-tRNA ligas
20	34	75.6	211	2	S12252	self incompatibili
21	34	75.6	330	2	AC0223	flagellar motor sw
22	34	75.6	331	2	F90963	flagellar motor sw
23	34	75.6	331	2	H64957	flagellar motor sw
24	34	75.6	708	2	T03835	vacA protein - sli
25	33	73.3	113	2	G90223	DNA-directed RNA p
26	33	73.3	223	2	F83703	hypothetical prote
27	33	73.3	345	1	JH0185	D-amino-acid oxida
28	33	73.3	399	2	B96567	hypothetical prote
29	33	73.3	499	1	A40092	protein-tyrosine k
30	33	73.3	505	2	I37206	protein-tyrosine k
31	33	73.3	595	2	S72537	acr-2 protein - Ne
32	33	73.3	695	2	S66662	protein-glutamine
33	33	73.3	695	2	T37667	probable cytochrom
34	33	73.3	1010	2	S45389	probable membrane
35	32	71.1	286	2	G65082	Putative general s
36	32	71.1	371	2	F84826	probable MADS-box
37	32	71.1	392	2	S04205	protein-tyrosine k
38	32	71.1	405	2	T09359	hypothetical prote
39	32	71.1	448	2	S56260	probable membrane
40	32	71.1	451	2	T16481	hypothetical prote
41	32	71.1	499	2	H83254	probable MFS trans
42	32	71.1	505	2	H95946	phosphate uptake A
43	32	71.1	517	2	A43807	protein-tyrosine k
44	32	71.1	517	2	S24547	protein-tyrosine k
45	32	71.1	529	1	TVHUFR	protein-tyrosine k
46	32	71.1	536	2	S33569	protein-tyrosine k
47	32	71.1	537	1	TVHUSY	protein-tyrosine k
48	32	71.1	539	2	B49114	protein-tyrosine k
49	32	71.1	600	2	F71434	probable limonene
50	32	71.1	663	1	TVMVRR	protein-tyrosine k
51	32	71.1	855	2	JH0287	immune regulatory
52	32	71.1	978	2	G75516	maltooligosyltreha
53	32	71.1	1283	2	T28812	hypothetical prote
54	32	71.1	1465	2	A70199	hypothetical prote
55	31	68.9	72	2	AE0255	hypothetical phage
56	31	68.9	106	2	B87263	conserved hypothet
57	31	68.9	112	2	A53291	tetracenomycin-bio
58	31	68.9	142	2	C82728	succinate dehydrog
59	31	68.9	195	2	T03086	probable thymidine
60	31	68.9	234	2	T25026	hypothetical prote
61	31	68.9	267	2	JQ1752	hypothetical 30.6K
62	31	68.9	272	2	C86539	CT041 hypothetical
63	31	68.9	272	2	C72084	conserved hypothet
64	31	68.9	281	2	F69484	hypothetical prote
65	31	68.9	286	2	F81717	conserved hypothet
66	31	68.9	287	2	T35229	hypothetical prote
67	31	68.9	307	2	B72031	lipoic acid synthe
68	31	68.9	307	2	F86594	lipoate synthetase
69	31	68.9	326	2	G84329	hypothetical prote
70	31	68.9	369	2	B72327	dnaJ protein - The
71	31	68.9	435	2	AI2690	amide hydrolase [i
72	31	68.9	438	2	T45389	SecY, preprotein t
73	31	68.9	441	2	G70822	probable secY prot
74	31	68.9	449	2	AE2597	hypothetical prote
75	31	68.9	449	2	F97379	phoT protein U5922
76	31	68.9	451	2	E97472	6-aminohexanoate-d
77	31	68.9	453	2	D89760	conserved hypothet
78	31	68.9	455	2	E83332	toluate 1,2-dioxyg
79	31	68.9	456	2	E75196	hypothetical prote
80	31	68.9	468	2	T12725	terminase large ch
81	31	68.9	518	2	T19562	hypothetical prote
82	31	68.9	527	2	PN0114	microbial metallop
83	31	68.9	560	2	S51600	phosphorylase kina
84	31	68.9	574	2	T25887	hypothetical prote
85	31	68.9	581	2	F97184	DNA modification m
86	31	68.9	622	2	S54585	hypothetical prote
87	31	68.9	623	2	S73462	transport ATP-bind
88	31	68.9	659	2	S10228	parasporal crystal
89	31	68.9	778	2	F95188	cation-transportin
90	31	68.9	778	2	G98054	P-type ATPase, met
91	31	68.9	862	2	S64821	probable membrane
92	31	68.9	903	2	T09143	alpha-glucosidase
93	31	68.9	1131	2	T09701	phytochrome - Scot
94	31	68.9	1250	2	A96586	hypothetical prote
95	30	66.7	15	2	PQ0193	stylar glycoprotei
96	30	66.7	88	2	AH1367	B. subtilis YtnI p
97	30	66.7	88	2	AI1736	B. subtilis YtnI p
98	30	66.7	105	2	A70701	hypothetical prote
99	30	66.7	119	2	AC1227	hypothetical prote
100	30	66.7	119	2	AE1580	hypothetical prote

ALIGNMENTS

RESULT 1
I48845
protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse
N;Alternate names: p56; protein-tyrosine kinase tck
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I48845; A23639; I57629; I77452
R;Voronova, A.F.; Sefton, B.M.
Nature 319, 682-685, 1986
A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A;Reference number: I48845; MUID:86146842; PMID:3081813
A;Accession: I48845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-509 <VOR1>
A;Cross-references: UNIPROT:Q91X65; UNIPARC:UPI000000418D; EMBL:X03533; NID:g54813; PIDN
R;Marth, J.D.; Peet, R.; Krebs, E.G.; Perimutter, R.M.
Cell 43, 393-404, 1985
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres
A;Reference number: A23639; MUID:86079521; PMID:2416464
A;Accession: A23639
A;Molecule type: mRNA
A;Residues: 1-282,'VP',285-509 <MAR>
A;Cross-references: UNIPARC:UPI0000172586; GB:M12056; NID:g198763
A;Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB59674.1
R;Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
A;Title: Two lck transcripts containing different 5' untranslated regions are present in
A;Reference number: I57629; MUID:88142832; PMID:3501824
A;Accession: I57629
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <VOR>
A;Cross-references: UNIPARC:UPI000016CE9D; GB:M18098; NID:g198766; PIDN:AAA39421.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I77452
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <GAR>
A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match 100.0%; Score 45; DB 1; Length 509;
  Best Local Similarity 100.0%; Pred. No. 0.3;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
|||||||||
Db 486 TFDYLRSVL 494

RESULT 2
OKHULK
protein-tyrosine kinase (EC 2.7.1.112) lck - human
N;Alternate names: kinase-related transforming protein (lck)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Oct-2004
C;Accession: JQ0152; S07822; S07200; S01879; S07143; A32797; I57636
R;Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
Gene 84, 105-113, 1989
A;Title: Structure of the human lck gene: differences in genomic organisation within src
A;Reference number: JQ0152; MUID:90108697; PMID:2558056
A;Accession: JQ0152
A;Molecule type: DNA
A;Residues: 1-509 <ROU>
A;Cross-references: UNIPROT:P06239; UNIPARC:UPI0000151F17; EMBL:X14053
R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
J. Cell. Biochem. 38, 117-126, 1988
A;Title: Structure and expression of lck transcripts in human lymphoid cells.
A;Reference number: S07822; MUID:89123626; PMID:3265417
A;Accession: S07822
A;Molecule type: mRNA
A;Residues: 1-86,'P',88-509 <PER>
A;Cross-references: UNIPARC:UPI0000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID
R;Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
A;Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homol
A;Reference number: S07200; MUID:87133831; PMID:3493153
A;Accession: S07200
A;Molecule type: mRNA
A;Residues: 1-205,'ASAITPI',212-257,'RCGW',262,'TTT',266,'T',268-281,'AGRLP',287-503,'STA
A;Cross-references: UNIPARC:UPI000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID
R;Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987
A;Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other nc
A;Reference number: S01879; MUID:88217332; PMID:2835736
A;Accession: S01879
A;Molecule type: mRNA
A;Residues: 368-471,'H',473-509 <VEI>
A;Cross-references: UNIPARC:UPI000016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID
R;Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986
A;Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).
A;Reference number: S07143; MUID:87000726; PMID:3489486
A;Accession: S07143
A;Molecule type: mRNA
A;Residues: 'A',376-509 <TRE>
A;Cross-references: UNIPARC:UPI000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID
R;Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W
Mol. Cell. Biol. 9, 2173-2180, 1989
A;Title: Structure of the two promoters of the human lck gene: differential accumulation
A;Reference number: A32797; MUID:89313764; PMID:2787474
A;Accession: A32797
A;Molecule type: DNA
A;Residues: 1-35 <TAK>
A;Cross-references: UNIPARC:UPI000016ABFF; GB:M26692; NID:g341523; PIDN:AAA59503.1; PID:g
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I57636
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <RES>
A;Cross-references: UNIPARC:UPI000016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:g
C;Comment: Protein tyrosine kinases play important roles in the control of cell growth ar
C;Genetics:
A;Gene: GDB:LCK
A;Cross-references: GDB:119360; OMIM:153390
A;Map position: 1p35-1p34.3
A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,5/Binding site: palmitate (Cys) (covalent) #status predicted

```
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             100.0%;  Score 45;  DB 1;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        486 TFDYLRSVL 494


RESULT 3
A39719
protein-tyrosine kinase (EC 2.7.1.112) lyn, long splice form - mouse
N;Contains: protein-tyrosine kinase lyn, short splice form
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: A39719; B39719; A39750; B39750
R;Stanley, E.; Ralph, S.; McEwen, S.; Boulet, I.; Holtzman, D.A.; Lock, P.; Dunn, A.R.
Mol. Cell. Biol. 11, 3399-3406, 1991
A;Title: Alternatively spliced murine lyn mRNAs encode distinct proteins.
A;Reference number: A39719; MUID:91260688; PMID:1710766
A;Accession: A39719
A;Molecule type: mRNA
A;Residues: 1-512 <STA1>
A;Cross-references: UNIPROT:P25911; UNIPARC:UPI000016CEBE; GB:M64608; NID:g198938; PIDN:
A;Accession: B39719
A;Molecule type: mRNA
A;Residues: 1-24,46-512 <STA2>
A;Cross-references: UNIPARC:UPI0000172584; GB:M64608
R;Yi, T.; Bolen, J.B.; Ihle, J.N.
Mol. Cell. Biol. 11, 2391-2398, 1991
A;Title: Hematopoietic cells express two forms of lyn kinase differing by 21 amino acids
A;Reference number: A39750; MUID:91203857; PMID:2017160
A;Accession: A39750
A;Molecule type: mRNA
A;Residues: 1-76,'F',78-160,'I',162-278,'L',280-390,'I',392-424,'D',426-512 <YI1>
A;Cross-references: UNIPARC:UPI000016CEBF; GB:M57696; NID:g198940; PIDN:AAA39471.1; PID:
A;Accession: B39750
A;Molecule type: mRNA
A;Residues: 1-24,46-76,'F',78-160,'I',162-278,'L',280-390,'I',392-424,'D',426-512 <YI2>
A;Cross-references: UNIPARC:UPI000016CEC0; GB:M57697; NID:g198942; PIDN:AAA39472.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F;1-512/Product: protein-tyrosine kinase lyn, long splice form #status predicted <MATL>
F;1-24,46-512/Product: protein-tyrosine kinase lyn, short splice form #status predicted
F;70-118/Domain: SH3 homology <SH3>
F;129-226/Domain: SH2 homology <SH2>
F;245-504/Domain: protein kinase homology <KIN>
F;253-261/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;275/Active site: Lys #status predicted
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             91.1%;  Score 41;  DB 1;  Length 512;
  Best Local Similarity   88.9%;  Pred. No. 2;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        489 TFDYLQSVL 497


RESULT 4
I56160
protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat
N;Contains: protein-tyrosine kinase lyn, splice form B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I56160; I67811; I67812
R;Minoguchi, K.; Nishikata, H.; Siraganian, R.P.
J. Immunol. 150, 222, 1993
A;Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leuke
A;Reference number: I56160
A;Accession: I56160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <MIN>
A;Cross-references: UNIPROT:Q07014; UNIPARC:UPI0000167AC2; GB:L14951; NID:g294582; PIDN:
R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
Gene 138, 219-222, 1994
A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed i
A;Reference number: I53715; MUID:94171041; PMID:8125304
A;Accession: I67811
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230,'L',232-307,'A',309-418,'Y',420-512 <RID1>
A;Cross-references: UNIPARC:UPI0000170BE3; GB:L14782; NID:g294578; PIDN:AAA20944.1; PID:
A;Note: in Genbank entry RATLYNATYR, release 116.0, PIDN:AAA20944.1, the source is desig
A;Accession: I67812
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-24,46-230,'L',232-307,'A',309-418,'Y',420-512 <RID2>
A;Cross-references: UNIPARC:UPI0000170BE2; GB:L14823; NID:g294580; PIDN:AAA20945.1; PID:
A;Note: in Genbank entry RATLYNBTYR, release 116.0, PIDN:AAA20945.1, the source is desig
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F;2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>
F;2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT
F;70-118/Domain: SH3 homology <SH3>
F;129-226/Domain: SH2 homology <SH2>
F;245-504/Domain: protein kinase homology <KIN>
F;253-261/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;275/Active site: Lys #status predicted
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             91.1%;  Score 41;  DB 1;  Length 512;
  Best Local Similarity   88.9%;  Pred. No. 2;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        489 TFDYLQSVL 497


RESULT 5
TVHULY
protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - human
N;Contains: protein-tyrosine kinase lyn, splice form B
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 05-Oct-2004
C;Accession: A26719; D38268; PH0949; I53715
R;Yamanashi, Y.; Fukushige, S.I.; Semba, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.;
Mol. Cell. Biol. 7, 237-243, 1987
A;Title: The yes-related cellular gene lyn encodes a possible tyrosine kinase similar to
A;Reference number: A26719; MUID:87172710; PMID:3561390
A;Accession: A26719
A;Molecule type: mRNA
A;Residues: 1-512 <YAM>
A;Cross-references: UNIPROT:P07948; UNIPARC:UPI000013DACD; GB:M16038; NID:g187268; PIDN:
R;Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: D38268
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 369-424 <PAR>
A;Cross-references: UNIPARC:UPI0000172583
R;Bielke, W.; Ziemieki, A.; Kappos, L.; Miescher, G.C.
Biochem. Biophys. Res. Commun. 186, 1403-1409, 1992
A;Title: Expression of the B cell-associated tyrosine kinase gene lyn in primary neurobl
A;Reference number: PH0949; MUID:92378604; PMID:1510669
A;Accession: PH0949
```

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A;Molecule type: mRNA
A;Residues: 369-424 <BIE>
A;Cross-references: UNIPARC:UPI0000172583
A;Experimental source: neuroblastoma SK-IN cell
R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
Gene 138, 219-222, 1994
A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed i
A;Reference number: I53715; MUID:94171041; PMID:8125304
A;Accession: I53715
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-24,46-512 <RID>
A;Cross-references: UNIPARC:UPI000016AC37; GB:M79321; NID:g187270; PIDN:AAB50019.1; PID:
A;Experimental source: splice form B
C;Genetics:
A;Gene: GDB:LYN
A;Cross-references: GDB:120159; OMIM:165120
A;Map position: 8q13-8qter
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
yrosine-specific protein kinase
F;2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>
F;2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT
F;70-118/Domain: SH3 homology <SH3>
F;129-226/Domain: SH2 homology <SH2>
F;245-504/Domain: protein kinase homology <KIN>
F;253-261/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;275/Active site: Lys #status predicted
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             91.1%;  Score 41;  DB 1;  Length 512;
  Best Local Similarity   88.9%;  Pred. No. 2;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        489 TFDYLQSVL 497


RESULT 6
AF2409
mannosyl transferase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2409
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2409
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <KUR>
A;Cross-references: UNIPROT:Q8YMU7; UNIPARC:UPI00000CEC79; GB:BA000019; PIDN:BAB76529.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4830
C;Superfamily: hypothetical protein sll1534

  Query Match             82.2%;  Score 37;  DB 2;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 9.6;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRS 7
              |||||||
Db        124 TFDYLRS 130


RESULT 7
TVHAST
protein-tyrosine kinase (EC 2.7.1.112) stk - Hydra attenuata
C;Species: Hydra attenuata
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004
C;Accession: A34094
R;Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E.
Mol. Cell. Biol. 9, 4141-4151, 1989
A;Title: Structure and expression of STK, a src-related gene in the simple metazoan Hydra
A;Reference number: A34094; MUID:90066418; PMID:2479820
A;Accession: A34094
A;Molecule type: mRNA
A;Residues: 1-509 <BOS>
A;Cross-references: UNIPROT:P17713; UNIPARC:UPI000013610D; GB:M25245; NID:g159273; PIDN:A
C;Genetics:
A;Gene: stk
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology,
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
F;66-115/Domain: SH3 homology <SH3>
F;126-218/Domain: SH2 homology <SH2>
F;238-497/Domain: protein kinase homology <KIN>
F;246-254/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;4/Binding site: palmitate (Cys) (covalent) #status predicted
F;268/Active site: Lys #status predicted
F;390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             82.2%;  Score 37;  DB 1;  Length 509;
  Best Local Similarity   77.8%;  Pred. No. 13;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||: ||
Db        482 TFDYLQGVL 490


RESULT 8
JC5604
ABC-transporting peroxisomal membrane protein 69 - human
C;Species: Homo sapiens (man)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 05-Oct-2004
C;Accession: JC5604
R;Holzinger, A.; Kammerer, S.; Roscher, A.A.
Biochem. Biophys. Res. Commun. 237, 152-157, 1997
A;Title: Primary structure of human PMP69, a putative peroxisomal ABC-transporter.
A;Reference number: JC5604; MUID:97410133; PMID:9266848
A;Accession: JC5604
A;Molecule type: mRNA
A;Residues: 1-606 <HOL>
A;Cross-references: UNIPROT:O14678; UNIPARC:UPI000004C4C8; DDBJ:AF009746; NID:g2343156;
C;Comment: This protein is a heterodimer partner of peroxisomal protein 70 and plays a r
C;Genetics:
A;Map position: 14q24.3
C;Keywords: ATP; nucleotide binding; P-loop; peroxisome
F;404-594/Domain: ATP-binding cassette homology <ABC>
F;421-428/Region: nucleotide-binding motif A (P-loop)

  Query Match             82.2%;  Score 37;  DB 2;  Length 606;
  Best Local Similarity   77.8%;  Pred. No. 16;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              ||||| |:|
Db        276 TFDYLGSIL 284


RESULT 9
T09672
ent-kaurene synthase B (EC 2.5.1.-) - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09672
```

R;Yamaguchi, S.; Saito, T.; Abe, H.; Yamane, H.; Murofushi, N.; Kamiya, Y.
Plant J. 10, 203-213, 1996
A;Title: Molecular cloning and characterization of a cDNA encoding the gibberellin biosy
A;Reference number: Z16814; MUID:96367664; PMID:8771778
A;Accession: T09672
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-789 <YAM>
A;Cross-references: UNIPROT:Q39548; UNIPARC:UPI00000ACCF3; EMBL:U43904; NID:g1431869; PI
A;Experimental source: immature seeds
C;Function:
A;Description: catalyzes the conversion of copalyl diphosphate to ent-kaurene
A;Pathway: gibberellin biosynthesis
A;Note: terpene cyclase
C;Superfamily: terpene synthase
C;Keywords: transferase

Query Match 82.2%; Score 37; DB 2; Length 789;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FDYLRSVL 9
||||||:|
Db 253 FDYLRSLL 260

RESULT 10
C81658
lipoic acid synthetase TC0847 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Dec-2004
C;Accession: C81658
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: C81658
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 <TET>
A;Cross-references: UNIPROT:Q9PJI2; UNIPARC:UPI0000057AA5; GB:AE002351; GB:AE002160; NID
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0847
C;Superfamily: lipoyl synthase

Query Match 80.0%; Score 36; DB 2; Length 308;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TFDYLRSV 8
||||.|||
Db 263 TFDYYRSV 270

RESULT 11
F71500
probable lipoate synthetase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 31-Dec-2004
C;Accession: F71500
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: F71500
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <ARN>
A;Cross-references: UNIPROT:O84562; UNIPARC:UPI000012E6C5; GB:AE001326; GB:AE001273; NID
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: lipA
C;Superfamily: lipoyl synthase

Query Match 80.0%; Score 36; DB 2; Length 311;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TFDYLRSV 8
||||.|||
Db 262 TFDYYRSV 269

RESULT 12
A39939
protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
N;Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
C;Species: Gallus gallus (chicken)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A42126; A39939
R;Chow, L.M.; Ratcliffe, M.J.; Veillette, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A;Reference number: A42126; MUID:92186854; PMID:1545804
A;Accession: A42126
A;Molecule type: mRNA
A;Residues: 1-88 <CHO>
A;Cross-references: UNIPARC:UPI0000172587; GB:M85043
A;Experimental source: thymus, spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
R;Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate
A;Reference number: A39939; MUID:88097370; PMID:3321053
A;Accession: A39939
A;Molecule type: mRNA
A;Residues: 52-507 <STR>
A;Cross-references: UNIPARC:UPI00001713B3; GB:J03579; NID:g212712; PIDN:AAA49081.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;66-114/Domain: SH3 homology <SH3>
F;125-222/Domain: SH2 homology <SH2>
F;241-499/Domain: protein kinase homology <KIN>
F;249-257/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 80.0%; Score 36; DB 1; Length 507;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9
||:|::|||
Db 484 TFEYMKSVL 492

RESULT 13
T09079
probable chloroquine resistance protein CG2 (strain 7G8) - malaria parasite (Plasmodium
C;Species: Plasmodium falciparum
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T09079
R;Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellems, T.E.
Cell 91, 593-603, 1997
A;Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
A;Reference number: Z16556; MUID:98054002; PMID:9393853
A;Accession: T09079
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2708 <SUX>
A;Cross-references: UNIPROT:O15791; UNIPARC:UPI0000079A61; EMBL:AF030692; NID:g2642513;
A;Experimental source: strain 7G8; from Brazil
C;Genetics:
A;Gene: cg2

```
C;Keywords: toxin resistance

  Query Match             80.0%;  Score 36;  DB 2;  Length 2708;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 FDYLRSVL 9
              |||||| |
Db         48 FDYLRSAL 55


RESULT 14
T09080
probable chloroquine resistance protein CG2 (strain HB3) - malaria parasite (Plasmodium
C;Species: Plasmodium falciparum
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T09080
R;Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellems, T.E.
Cell 91, 593-603, 1997
A;Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
A;Reference number: Z16556; MUID:98054002; PMID:9393853
A;Accession: T09080
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2819 <SUX>
A;Cross-references: UNIPROT:O15792; UNIPARC:UPI00000785E5; EMBL:AF030693; NID:g2642515;
A;Experimental source: strain HB3; from Honduras
C;Genetics:
A;Gene: cg2
C;Keywords: toxin resistance

  Query Match             80.0%;  Score 36;  DB 2;  Length 2819;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 FDYLRSVL 9
              |||||| |
Db         48 FDYLRSAL 55


RESULT 15
T27697
VPS29-like phosphoesterase-related protein ZK1128.8 [similarity] - Caenorhabditis elegan
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27697
R;Berks, M.
submitted to the EMBL Data Library, January 1995
A;Reference number: Z20407
A;Accession: T27697
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-157 <WIL>
A;Cross-references: UNIPROT:Q9XVX5; UNIPARC:UPI000007FB10; EMBL:Z47357; PIDN:CAA87426.1;
A;Experimental source: clone ZK1128
C;Genetics:
A;Gene: CESP:ZK1128.8
A;Map position: 3
A;Introns: 20/2; 68/3
C;Superfamily: VPS29-like phosphoesterase-related protein; phosphoesterase core homology

  Query Match             77.8%;  Score 35;  DB 2;  Length 157;
  Best Local Similarity   75.0%;  Pred. No. 9.6;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSV 8
              ||||||::
Db         15 TFDYLRTL 22


RESULT 16
JQ1321
protein-tyrosine kinase (EC 2.7.1.112) hck - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: JQ1321; S18974
R;Okano, Y.; Sugimoto, Y.; Fukuoka, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
A;Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes.
A;Reference number: JQ1321; MUID:92109719; PMID:1764064
A;Accession: JQ1321
A;Molecule type: mRNA
A;Residues: 1-503 <OKA>
A;Cross-references: UNIPROT:P50545; UNIPARC:UPI000012C350; GB:S74141; NID:g241436; PIDN:A
A;Experimental source: megakaryocyte
R;Rema, V.; Swarup, G.
submitted to the EMBL Data Library, December 1991
A;Reference number: S18974
A;Accession: S18974
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-50,'V',52-204,'R',206-305,'T',307-503 <REM>
A;Cross-references: UNIPARC:UPI0000170BD7; EMBL:X62345; NID:g57581; PIDN:CAA44218.1; PID
C;Genetics:
A;Gene: hck
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology,
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming prot
n kinase
F;62-110/Domain: SH3 homology <SH3>
F;121-218/Domain: SH2 homology <SH2>
F;237-495/Domain: protein kinase homology <KIN>
F;245-253/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;267/Active site: Lys #status predicted
F;388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             77.8%;  Score 35;  DB 1;  Length 503;
  Best Local Similarity   66.7%;  Pred. No. 33;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              ||:|::|||
Db        480 TFEYIQSVL 488


RESULT 17
TVMSHC
protein-tyrosine kinase (EC 2.7.1.112) hck - mouse
N;Alternate names: kinase-related transforming protein (bmk)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A27282; A39973
R;Klemsz, M.J.; McKercher, S.R.; Maki, R.A.
Nucleic Acids Res. 15, 9600, 1987
A;Title: Nucleotide sequence of the mouse hck gene.
A;Reference number: A27282; MUID:88067781; PMID:3684607
A;Accession: A27282
A;Molecule type: mRNA
A;Residues: 1-503 <KLE>
A;Cross-references: UNIPROT:P08103; UNIPARC:UPI00000018DD; GB:Y00487; NID:g51209; PIDN:C
R;Holtzman, D.A.; Cook, W.D.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
A;Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed
A;Reference number: A39973; MUID:88068587; PMID:3317404
A;Accession: A39973
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-503 <HOL>
A;Cross-references: UNIPARC:UPI00000018DD; GB:J03023; NID:g192212; PIDN:AAA37305.1; PID:
C;Genetics:
A;Gene: hck
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;62-110/Domain: SH3 homology <SH3>
F;121-218/Domain: SH2 homology <SH2>
```

F;237-495/Domain: protein kinase homology <KIN>
F;245-253/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;267/Active site: Lys #status predicted
F;388,499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 77.8%; Score 35; DB 1; Length 503;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFDYLRSVL 9
              ||:|::|||
Db        480 TFEYIQSVL 488
```

RESULT 18
TVHUHC
protein-tyrosine kinase (EC 2.7.1.112) hck - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: A27811; A27812; JC1149; C38268; S31103
R;Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Dia
Mol. Cell. Biol. 7, 2267-2275, 1987
A;Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and
A;Reference number: A27811; MUID:87257942; PMID:3496523
A;Accession: A27811
A;Molecule type: mRNA
A;Residues: 1-505 <QUI>
A;Cross-references: UNIPROT:P08631; UNIPARC:UPI000015C528; GB:M16591
A;Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation
R;Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.
Mol. Cell. Biol. 7, 2276-2285, 1987
A;Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of h
A;Reference number: A27812; MUID:87257943; PMID:3453117
A;Accession: A27812
A;Molecule type: mRNA
A;Residues: 1-505 <ZIE>
A;Cross-references: UNIPARC:UPI000015C528; GB:M16592; NID:g183913; PIDN:AAA52644.1; PID:
R;Hradetzky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Gene 113, 275-280, 1992
A;Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinas
A;Reference number: JC1149; MUID:92241680; PMID:1572549
A;Accession: JC1149
A;Molecule type: DNA
A;Residues: 157-505 <HRA>
A;Cross-references: UNIPARC:UPI0000172589; EMBL:X59741
R;Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: C38268
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 362-417 <PAR>
A;Cross-references: UNIPARC:UPI000017258A
C;Genetics:
A;Gene: GDB:HCK
A;Cross-references: GDB:119303; OMIM:142370
A;Map position: 20q11-20q12
A;Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-505/Product: protein-tyrosine kinase hck #status predicted <MAT>
F;64-112/Domain: SH3 homology <SH3>
F;123-220/Domain: SH2 homology <SH2>
F;239-497/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;269/Active site: Lys #status predicted
F;390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 77.8%; Score 35; DB 1; Length 505;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFDYLRSVL 9
              ||:|::|||
Db        482 TFEYIQSVL 490
```

RESULT 19
H71647
alanine-tRNA ligase (EC 6.1.1.7) (alaS) RP856 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: H71647
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: H71647
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-877 <AND>
A;Cross-references: UNIPROT:Q9ZCA4; UNIPARC:UPI0000136321; GB:AJ235273; GB:AJ235269; NID
A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: alaS; RP856
C;Superfamily: alanyl-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 77.8%; Score 35; DB 2; Length 877;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TFDYLRSVL 9
              || ||||::
Db        526 TFKYLRSII 534
```

RESULT 20
S12252
self incompatibility-associated protein precursor, pistil-specific (allele S2) - Chaco p
N;Alternate names: probable ribonuclease S2
C;Species: Solanum chacoense (Chaco potato)
C;Date: 21-Nov-1993 #sequence_revision 24-May-1996 #text_change 31-Dec-2004
C;Accession: S12252; S64639
R;Xu, B.; Mu, J.; Nevins, D.L.; Grun, P.; Kao, T.
Mol. Gen. Genet. 224, 341-346, 1990
A;Title: Cloning and sequencing of cDNAs encoding two self-incompatibility associated pr
A;Reference number: S12252; MUID:91094770; PMID:2266940
A;Accession: S12252
A;Molecule type: mRNA
A;Residues: 1-211 <XUB>
A;Cross-references: UNIPROT:Q06026; UNIPARC:UPI00000ABEBC; EMBL:X56896; NID:g288518; PID
A;Accession: S64639
A;Molecule type: protein
A;Residues: 15-29 <XUW>
A;Cross-references: UNIPARC:UPI0000175A14
C;Superfamily: RNases
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-211/Product: self incompatibility-associated protein #status experimental <MAT>

Query Match 75.6%; Score 34; DB 2; Length 211;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TFDYLRSVL 9
              ||||:: ||
Db         15 TFDYMKLVL 23
```

```
RESULT 21
AC0223
flagellar motor switch protein FliG [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0223
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0223
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-330 <KUR>
A;Cross-references: UNIPROT:Q8ZF87; UNIPARC:UPI00000DCCE9; GB:AL590842; PIDN:CAC90647.1;
C;Genetics:
A;Gene: fliG
C;Superfamily: flagellar switch protein fliG

  Query Match             75.6%;  Score 34;  DB 2;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 DYLRSVL 9
              |||||||
Db         74 DYLRSVL 80


RESULT 22
F90963
flagellar motor switch protein FliG [imported] - Escherichia coli (strain O157:H7, subst
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90963
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90963
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <HAY>
A;Cross-references: UNIPROT:P31067; UNIPARC:UPI000012A9AF; GB:BA000007; PIDN:BAB36101.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2678
C;Superfamily: flagellar switch protein fliG

  Query Match             75.6%;  Score 34;  DB 2;  Length 331;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 DYLRSVL 9
              |||||||
Db         75 DYLRSVL 81


RESULT 23
H64957
flagellar motor switch protein fliG - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: H64957; JN0905
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64957
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-331 <BLAT>
A;Cross-references: UNIPROT:P31067; UNIPARC:UPI000012A9AF; GB:AE000286; GB:U00096; NID:g1
A;Experimental source: strain K-12, substrain MG1655
R;Roman, S.J.; Frantz, B.B.; Matsumura, P.
Gene 133, 103-108, 1993
A;Title: Gene sequence, overproduction, purification and determination of the wild-type
A;Reference number: JN0905; MUID:94040782; PMID:8224881
A;Accession: JN0905
A;Molecule type: DNA
A;Residues: 1-13,15-35,'RV',38-158,'F','VSHLWRRA',169,'S',171-331 <ROM>
A;Cross-references: UNIPARC:UPI00001783AE
C;Genetics:
A;Gene: fliG
C;Function:
A;Description: part of the flagellar switch mediating flagella rotation during chemotaxi
A;Note: there are three switch proteins (fliG, fliM, fliN) which together determine the c
C;Superfamily: flagellar switch protein fliG
C;Keywords: chemotaxis; flagellar rotation; flagellum

  Query Match             75.6%;  Score 34;  DB 2;  Length 331;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 DYLRSVL 9
              |||||||
Db         75 DYLRSVL 81


RESULT 24
T03835
vacA protein - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostelium discoideum
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03835
R;Shaulsky, G.; Loomis, W.F.
submitted to the EMBL Data Library, July 1997
A;Reference number: Z15108
A;Accession: T03835
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-708 <SHA>
A;Cross-references: UNIPROT:O15715; UNIPARC:UPI0000007945B; EMBL:AF015565; NID:g2353180;
A;Experimental source: train AX4
C;Genetics:
A;Gene: vacA

  Query Match             75.6%;  Score 34;  DB 2;  Length 708;
  Best Local Similarity   55.6%;  Pred. No. 77;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              :|||:| :|
Db        147 SFDYIREIL 155


RESULT 25
G90223
DNA-directed RNA polymerase, subunit F (rpoF) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Mar-2004
C;Accession: G90223
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90223
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <KUR>
A;Cross-references: UNIPARC:UPI0000066A98; GB:AE006641; NID:g13813918; PIDN:AAK41046.1;
```

```
C;Genetics:
A;Gene: rpoF
C;Superfamily: RNA polymerase, subunit F

  Query Match             73.3%;  Score 33;  DB 2;  Length 113;
  Best Local Similarity   75.0%;  Pred. No. 17;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSV 8
              |:||| ||
Db         37 TYDYLNSV 44


RESULT 26
F83703
hypothetical protein BH0430 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
C;Accession: F83703
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83703
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-223 <STO>
A;Cross-references: UNIPROT:Q9KFP8; UNIPARC:UPI00000C3895; GB:AP001508; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0430
C;Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase

  Query Match             73.3%;  Score 33;  DB 2;  Length 223;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLR 6
              ||||||
Db         26 TFDYLR 31


RESULT 27
JH0185
D-amino-acid oxidase (EC 1.4.3.3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH0185
R;Tada, M.; Fukui, K.; Momoi, K.; Miyake, Y.
Gene 90, 293-297, 1990
A;Title: Cloning and expression of a cDNA encoding mouse kidney D-amino acid oxidase.
A;Reference number: JH0185; MUID:90382679; PMID:1976103
A;Accession: JH0185
A;Molecule type: mRNA
A;Residues: 1-345 <TAD>
A;Cross-references: UNIPROT:P18894; UNIPARC:UPI000016CE73; GB:M32299; NID:g198571; PIDN:
A;Experimental source: kidney, strain BALB/c
C;Comment: D-Amino-acid oxidase is a flavoprotein associated with FAD which catalyzes th
C;Superfamily: D-amino-acid oxidase
C;Keywords: oxidoreductase
F;7-12/Domain: FAD binding #status predicted <FAD>
F;343-345/Region: peroxisome/glyoxysome location signal (S-[RKH]-L) motif
F;54,209,215/Active site: Tyr, Lys, His #status predicted

  Query Match             73.3%;  Score 33;  DB 1;  Length 345;
  Best Local Similarity   77.8%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              ||||| | |
Db         70 TFDYLLSCL 78


RESULT 28
B96567
hypothetical protein F6D8.15 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C;Accession: B96567
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96567
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <STO>
A;Cross-references: UNIPROT:Q9SSR5; UNIPARC:UPI00000AA1F0; GB:AE005173; NID:g5903043; PI
C;Genetics:
A;Gene: F6D8.15
A;Map position: 1
C;Superfamily: Similar to auxin-independent growth promoter (Axi 1)

  Query Match             73.3%;  Score 33;  DB 2;  Length 399;
  Best Local Similarity   75.0%;  Pred. No. 67;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 FDYLRSVL 9
              |||: |||
Db        128 FDYIESVL 135


RESULT 29
A40092
protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A40092
R;Dymecki, S.M.; Niederhuber, J.E.; Desiderio, S.V.
Science 247, 332-336, 1990
A;Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.
A;Reference number: A40092; MUID:90117147; PMID:2404338
A;Accession: A40092
A;Molecule type: mRNA
A;Residues: 1-499 <DYM>
A;Cross-references: UNIPROT:P16277; UNIPARC:UPI0000151F18; GB:M30903; NID:g202076; PIDN:
C;Genetics:
A;Gene: MGI:Blk
A;Cross-references: MGI:88169
A;Map position: 14:28.0
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;59-107/Domain: SH3 homology <SH3>
F;118-214/Domain: SH2 homology <SH2>
F;233-491/Domain: protein kinase homology <KIN>
F;241-249/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;263/Active site: Lys #status predicted

  Query Match             73.3%;  Score 33;  DB 1;  Length 499;
  Best Local Similarity   66.7%;  Pred. No. 84;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              ||::|:|||
Db        476 TFEFLQSVL 484


RESULT 30
```

```
I37206
protein-tyrosine kinase (EC 2.7.1.112) blk - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
C;Accession: I37206; S51647
R;Islam, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.
J. Immunol. 154, 1265-1272, 1995
A;Title: Molecular cloning, characterization, and chromosomal localization of a human ly
A;Reference number: I37206; MUID:95123078; PMID:7822795
A;Accession: I37206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-505 <RES>
A;Cross-references: UNIPROT:P51451; UNIPARC:UPI0000163B22; EMBL:Z33998; NID:g601951; PID
C;Genetics:
A;Gene: GDB:BLK
A;Cross-references: GDB:454114; OMIM:191305
A;Map position: 8p23-8p22
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
F;65-113/Domain: SH3 homology <SH3>
F;124-220/Domain: SH2 homology <SH2>
F;239-497/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;269/Active site: Lys #status predicted

  Query Match             73.3%;  Score 33;  DB 2;  Length 505;
  Best Local Similarity   66.7%;  Pred. No. 86;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              ||::|:|||
Db        482 TFEFLQSVL 490


Search completed: June 29, 2006, 09:31:35
Job time : 15.3373 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 97.5904 Seconds
(without alignments)
46.851 Million cell updates/sec

Title: US-10-062-257A-2
Perfect score: 51
Sequence: 1 DYLRSVLEDF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	4	AAG68080	Aag68080 Antitumou
2	51	100.0	10	4	AAB73118	Aab73118 Tumour an
3	51	100.0	10	6	ABR84377	Abr84377 Human lck
4	51	100.0	10	8	ADS87118	Ads87118 Human gen
5	51	100.0	10	9	ADX58316	Adx58316 Partial a
6	51	100.0	10	9	ADZ42231	Adz42231 Cytotoxic
7	51	100.0	10	9	AEC33133	Aec33133 Lck tumor
8	51	100.0	10	10	AEE99214	Aee99214 Cancer an
9	51	100.0	13	4	AAB73144	Aab73144 Tumour an
10	51	100.0	246	4	ABG22263	Abg22263 Novel hum
11	51	100.0	259	2	AAY43955	Aay43955 Human pro
12	51	100.0	263	8	ADR88385	Adr88385 LCK tyros
13	51	100.0	265	7	ABR56203	Abr56203 Mutant Ly
14	51	100.0	271	7	ABR56204	Abr56204 Mutant Ly
15	51	100.0	279	9	ADY85449	Ady85449 Catalytic
16	51	100.0	346	3	AAY76750	Aay76750 Human pro
17	51	100.0	346	4	AAE06208	Aae06208 Human pro
18	51	100.0	346	5	ABB84435	Abb84435 Human pro
19	51	100.0	355	8	ABM82980	Abm82980 Human dia
20	51	100.0	417	2	AAR14201	Aar14201 (Beta-gal
21	51	100.0	458	7	ADC99048	Adc99048 Human KPP
22	51	100.0	502	5	AAE21689	Aae21689 Fugu rubr
23	51	100.0	508	3	AAB37700	Aab37700 Human lym
24	51	100.0	508	7	ADE58802	Ade58802 Human Pro
25	51	100.0	508	7	ADE58799	Ade58799 Human Pro
26	51	100.0	508	7	ADF45072	Adf45072 Human kin
27	51	100.0	508	7	ADL34479	Adl34479 Human lym
28	51	100.0	508	8	ADS88148	Ads88148 Human pro
29	51	100.0	509	3	AAY49420	Aay49420 PKA subst
30	51	100.0	509	6	ABR58699	Abr58699 Human can
31	51	100.0	509	7	ABR56202	Abr56202 Human Lym
32	51	100.0	509	7	ADE40449	Ade40449 Human pro
33	51	100.0	509	8	ADL22907	Adl22907 Human MP2
34	51	100.0	509	8	ADP12458	Adp12458 Protein e
35	51	100.0	509	8	ADP48374	Adp48374 Human lym
36	51	100.0	509	9	ADZ51107	Adz51107 Amino aci
37	51	100.0	509	9	AEA35921	Aea35921 Human Lck
38	51	100.0	539	8	ABM82981	Abm82981 Human dia
39	51	100.0	539	8	ABM82982	Abm82982 Human dia
40	51	100.0	551	4	ABG22264	Abg22264 Novel hum
41	51	100.0	567	5	ABG79673	Abg79673 Tumour in
42	48	94.1	259	2	AAY43956	Aay43956 Mouse pro
43	44	86.3	13	4	AAB73149	Aab73149 Tumour an
44	44	86.3	260	2	AAY43954	Aay43954 Human pro
45	44	86.3	439	9	ADY52636	Ady52636 Human tra
46	44	86.3	440	9	ADY52635	Ady52635 Human tra
47	44	86.3	444	9	ADY52634	Ady52634 Human tra
48	44	86.3	447	9	ADY52633	Ady52633 Human tra
49	44	86.3	452	9	ADY52632	Ady52632 Human tra
50	44	86.3	459	9	ADY52631	Ady52631 Human tra
51	44	86.3	467	9	ADY52630	Ady52630 Human tra
52	44	86.3	472	9	ADY52629	Ady52629 Human tra
53	44	86.3	473	9	ADY52628	Ady52628 Human tra
54	44	86.3	481	9	ADY52627	Ady52627 Human tra
55	44	86.3	483	9	ADY52626	Ady52626 Human tra
56	44	86.3	493	9	ADY52625	Ady52625 Human tra
57	44	86.3	511	7	ADF45073	Adf45073 Human kin
58	44	86.3	512	7	ADD19014	Add19014 Human dis
59	44	86.3	512	7	ADN95430	Adn95430 Human BEC
60	44	86.3	512	8	ADL22908	Adl22908 Human MP2
61	44	86.3	512	8	ADN04498	Adn04498 Antipsori
62	44	86.3	512	8	ADP12483	Adp12483 Protein e
63	44	86.3	512	8	ADR14269	Adr14269 Human NF-
64	44	86.3	512	8	ADS88430	Ads88430 Human pro
65	44	86.3	512	8	ADP23372	Adp23372 PRO polyp
66	44	86.3	512	9	ADY16487	Ady16487 PRO polyp
67	44	86.3	512	9	ADY19685	Ady19685 PRO polyp
68	44	86.3	512	9	ADY14848	Ady14848 PRO polyp
69	44	86.3	512	9	ADY52574	Ady52574 Human onc
70	44	86.3	512	9	AEA35920	Aea35920 Human Lyn
71	42	82.4	496	2	AAY29668	Aay29668 Human src
72	42	82.4	496	4	AAU08734	Aau08734 Xenopus l
73	42	82.4	496	4	AAU08730	Aau08730 Xenopus l
74	42	82.4	496	4	AAU08735	Aau08735 Xenopus l
75	39	76.5	13	4	AAG68084	Aag68084 Antitumou
76	39	76.5	13	4	AAB73151	Aab73151 Tumour an
77	39	76.5	233	4	ABB71491	Abb71491 Drosophil
78	39	76.5	454	8	ADH48367	Adh48367 Human KPP
79	39	76.5	503	8	ADQ97514	Adq97514 Mouse can
80	39	76.5	504	7	ADF45035	Adf45035 Human kin
81	39	76.5	505	8	ADK70442	Adk70442 Respirato
82	39	76.5	505	8	ADL22909	Adl22909 Human MP2
83	39	76.5	505	8	ADQ97517	Adq97517 Human can
84	39	76.5	505	9	AEA35922	Aea35922 Human Blk
85	39	76.5	558	8	ADQ97519	Adq97519 Human can
86	38	74.5	13	4	AAG68083	Aag68083 Antitumou
87	38	74.5	13	4	AAB73147	Aab73147 Tumour an
88	38	74.5	13	4	AAB73150	Aab73150 Tumour an
89	38	74.5	259	2	AAY43957	Aay43957 Human pro
90	38	74.5	271	8	ADR88384	Adr88384 HCK tyros
91	38	74.5	272	5	ABB81188	Abb81188 Human KIT
92	38	74.5	300	9	ADY85468	Ady85468 Catalytic
93	38	74.5	316	9	ADY85448	Ady85448 Catalytic
94	38	74.5	383	7	ADJ68978	Adj68978 Human hea
95	38	74.5	436	8	ADN61468	Adn61468 Human KPP
96	38	74.5	438	9	ADY52642	Ady52642 Human tra

97	38	74.5	458	8	ADJ71657	Adj71657 Human NOV
98	38	74.5	463	7	ABO82621	Abo82621 Pseudomon
99	38	74.5	465	9	ADY52641	Ady52641 Human tra
100	38	74.5	471	9	ADY52640	Ady52640 Human tra

ALIGNMENTS

RESULT 1
AAG68080
ID AAG68080 standard; peptide; 10 AA.
XX
AC AAG68080;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide lck 488-497.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10
||||||||||
Db 1 DYLRSVLEDF 10

RESULT 2
AAB73118
ID AAB73118 standard; peptide; 10 AA.
XX
AC AAB73118;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #2.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 1; Page 66; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10
||||||||||
Db 1 DYLRSVLEDF 10

RESULT 3
ABR84377
ID ABR84377 standard; peptide; 10 AA.
XX
AC ABR84377;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human lck HLA-A24 epitope, SEQ ID NO:27.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.

XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 8; Page 10; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10
||||||||||
Db 1 DYLRSVLEDF 10

RESULT 4
ADS87118
ID ADS87118 standard; peptide; 10 AA.
XX
AC ADS87118;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genetic vaccine/ubiquitin (Ub)/Lck-related epitope peptide 3.
XX
KW vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
KW colon; bladder; breast; oesophagus; kidney; brain; human; epitope; Lck.
XX
OS Homo sapiens.
XX
PN WO2004035085-A1.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-JP013279.
XX
PR 17-OCT-2002; 2002JP-00302816.
XX
PA (KYUS-) KYUSHU TLO CO LTD.
XX
PI Himeno K, Furue M, Maehara Y;
XX
DR WPI; 2004-357144/33.
XX
PT Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
PT or cytokine genes for prevention and treatment of cancer.
XX
PS Disclosure; SEQ ID NO 134; 266pp; Japanese.
XX
CC The invention relates to a novel genetic vaccine containing the ubiquitin
CC gene together with a gene encoding an antigenic protein containing a T-
CC cell target sequence. The vaccine of the invention may be useful for
CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma
CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence
CC is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide
CC of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10
||||||||||
Db 1 DYLRSVLEDF 10

RESULT 5
ADX58316
ID ADX58316 standard; peptide; 10 AA.
XX
AC ADX58316;
XX
DT 21-APR-2005 (first entry)
XX
DE Partial antigenic peptide #2 derived from p56.
XX
KW cytostatic; vaccine; hematopoietic tumor; p56; immunotherapy.
XX
OS Unidentified.
XX
PN WO2005011723-A1.
XX
PD 10-FEB-2005.
XX
PF 05-AUG-2004; 2004WO-JP011232.
XX
PR 05-AUG-2003; 2003JP-00287208.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2005-152358/16.
XX
PT Prevention and/or therapeutic agent of hematopoietic tumor useful for
PT preventing and/or treating hematopoietic tumor, has peptides having amino
PT acid sequences of partial peptide of p56lck, SART-1, SART-2, SART-3, or
PT ART-1 protein.
XX
PS Claim 1; SEQ ID NO 2; 41pp; Japanese.
XX
CC The specification describes a remedy for a hematopoietic tumor. The
CC remedy comprises one or more peptides derived from p56 (lck), SART-1,
CC SART-2, SART-3, or ART-1 proteins as an active ingredient. The peptides
CC induce specific cytotoxic T cells. The remedy of thr invention is useful
CC for preventing and treating hematopoietic tumors comprising human
CC leukocyte antigen (HLA)-A24 molecules on its cell surface. It is also
CC useful in immunotherapy of hematopoietic tumors, and for treating
CC malignant tumors such as acute myelogenous leukemia, acute lymphoblastic
CC leukemia, chronic lymphocytic leukemia, malignant lymphoma, multiple
CC myeloma, etc. . The present sequence represents a partial peptide derived
CC from p56, and is used in the remedy of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10
||||||||||
Db 1 DYLRSVLEDF 10

```
RESULT 6
ADZ42231
ID   ADZ42231 standard; peptide; 10 AA.
XX
AC   ADZ42231;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Cytotoxic T-lymphocyte epitope peptide, Lck-488.
XX
KW   antibody; vaccine; immune stimulation; cytotoxic T-lymphocyte.
XX
OS   Synthetic.
XX
PN   JP2005099001-A.
XX
PD   14-APR-2005.
XX
PF   20-AUG-2004; 2004JP-00240269.
XX
PR   31-AUG-2003; 2003JP-00348853.
XX
PA   (ITOK/) ITO K.
PA   (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
XX
DR   WPI; 2005-310369/32.
XX
PT   Measuring anti-peptide antibody, by preparing supports immobilized with
PT   different peptides, pouring test substance comprising peptide recognizing
PT   antibody on supports, adding labeled secondary antibody, measuring amount
PT   of label.
XX
PS   Example 1; SEQ ID NO 7; 22pp; Japanese.
XX
CC   The invention relates to a novel method for measuring an anti-peptide
CC   antibody. The method involves preparing several supports immobilized with
CC   different kinds of peptides, pouring a test substance comprising a
CC   peptide recognizing antibody onto prepared supports for reacting a
CC   peptide with an antibody, combining the peptide recognizing antibody with
CC   a labeled secondary antibody, measuring the amount of coupled label and
CC   identifying the kind of support for measuring the anti-peptide antibody.
CC   The invention further comprises a method for selecting a peptide vaccine
CC   candidate. The method enables the measurement of anti-peptide antibodies
CC   from trace amounts of a sample, e.g. blood serum from patients, rapidly
CC   with high efficiency. The immune response specific to a peptide vaccine
CC   can be monitored efficiently. This sequence represents a cytotoxic T-
CC   lymphocyte (CTL) epitope peptide of the invention.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db          1 DYLRSVLEDF 10


RESULT 7
AEC33133
ID   AEC33133 standard; peptide; 10 AA.
XX
AC   AEC33133;
XX
DT   17-NOV-2005  (first entry)
XX
DE   Lck tumor antigen peptide SEQ ID NO 8.
XX
KW   cytostatic; vaccine; gene therapy; epitope; immunogenicity; diagnosis;
KW   tumor-associated antigen; cancer; neoplasm; Lck.
XX
OS   Homo sapiens.
XX
PN   WO2005083074-A1.
XX
PD   09-SEP-2005.
XX
PF   01-MAR-2005; 2005WO-JP003399.
XX
PR   01-MAR-2004; 2004JP-00056865.
XX
PA   (UYKA-) UNIV KANAZAWA TECHNOLOGY LICENSING ORG.
XX
PI   Kaneko S,  Mizukoshi E,  Nakamoto Y,  Tsuji H;
XX
DR   WPI; 2005-619189/63.
XX
PT   Novel tumor antigen peptide derived from Cyp-B, SART, p53, alpha-
PT   fetoprotein and human telomerase reverse transcriptase, useful for
PT   preparing anti-tumor peptide vaccine.
XX
PS   Example 1; SEQ ID NO 8; 58pp; Japanese.
XX
CC   The invention describes a tumor antigen peptide (I) including Cyp-B,
CC   SART, p53, multidrug resistance protein (MRP), alpha-fetoprotein (AFP) or
CC   human telomerase reverse transcriptase (hTERT) derived peptide comprising
CC   an amino acid sequence (S1) of SEQ ID No. 4, 14, 15, 18, 19, 23-25, 27-
CC   30, 34, 37-41 or 44. Also described are: an anti-tumor peptide vaccine
CC   comprising (I); antigen presenting cells (II) presenting (I), obtained by
CC   cultivating human leukocyte antigen (HLA)-A24 positive antigen presenting
CC   cells with (I); nucleic acid molecule (III) comprising a base sequence
CC   encoding (S1); an antibody (A1) capable of specifically binding to (I);
CC   inducing (M1) cytotoxic T cells, involves cultivating tumor tissue
CC   infiltrated lymphocyte or peripheral blood lymphocyte isolated from the
CC   HLA-A24 positive patient, with (I) and interleukin (IL)-2; and anti-tumor
CC   agent comprising (III) or the cytotoxic T cell acquired by (M1). (I) is
CC   useful for preparing anti-tumor peptide vaccine. The nucleic acid
CC   molecule is useful as an anti-tumor agent. The antibody is useful for
CC   detecting or diagnosing cancer. (I) is an effective immunogenic peptide
CC   with respect to tumor. This is the amino acid sequence of a Lck tumor
CC   antigen peptide. Note: This sequence is also available in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db          1 DYLRSVLEDF 10


RESULT 8
AEE99214
ID   AEE99214 standard; peptide; 10 AA.
XX
AC   AEE99214;
XX
DT   23-FEB-2006  (first entry)
XX
DE   Cancer antigen lck peptide SEQ ID NO 4.
XX
KW   Cytostatic; Vaccine; cancer; neoplasm; antigen; lck.
XX
OS   Unidentified.
XX
PN   WO2005123122-A1.
XX
PD   29-DEC-2005.
XX
PF   21-JUN-2005; 2005WO-JP011357.
```

XX
PR 21-JUN-2004; 2004JP-00182811.
XX
PA (UYKU-) UNIV KURUME.
XX
PI Itoh K;
XX
DR WPI; 2006-057212/06.
XX
PT Treating cancer by evaluating specific cytotoxic T-lymphocyte precursors
PT for each peptide of cancer antigen peptide set, in patient, administering
PT peptide set obtained after removing peptide being non-specific to
PT precursors, to patient.
XX
PS Example 1; SEQ ID NO 4; 36pp; Japanese.
XX
CC The invention relates to a method of treating a cancer patient by
CC administering cancer antigens to patient, involves evaluating presence or
CC absence of specific cytotoxic T-lymphocyte precursors for individual
CC peptides contained in set of cancer antigen peptides, in patient,
CC removing peptide being non-specific to precursors, from cancer antigen
CC peptide set, to prepare set for administration, and administering cancer
CC antigen peptide set to patient. The method is useful for treating cancer
CC patient by administering cancer antigens to patient. The present sequence
CC represents the amino acid sequence of a lck peptide cancer antigen.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10
||||||||||
Db 1 DYLRSVLEDF 10

RESULT 9
AAB73144
ID AAB73144 standard; peptide; 13 AA.
XX
AC AAB73144;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #28.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Example 6; Page 36; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 51; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10
||||||||||
Db 3 DYLRSVLEDF 12

RESULT 10
ABG22263
ID ABG22263 standard; protein; 246 AA.
XX
AC ABG22263;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22254.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86450.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 52622; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

```
SQ   Sequence 246 AA;

  Query Match             100.0%;  Score 51;  DB 4;  Length 246;
  Best Local Similarity   100.0%;  Pred. No. 0.6;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        225 DYLRSVLEDF 234


RESULT 11
AAY43955
ID   AAY43955 standard; protein; 259 AA.
XX
AC   AAY43955;
XX
DT   21-DEC-1999  (first entry)
XX
DE   Human protein kinase #15.
XX
KW   Prediction; secondary structure; alignment; evolutionary conservation;
KW   homology; periodicity; co-variation analysis; antigenic site;
KW   site directed mutagenesis; interaction.
XX
OS   Homo sapiens.
XX
PN   US5958784-A.
XX
PD   28-SEP-1999.
XX
PF   25-MAR-1992;   92US-00857224.
XX
PR   25-MAR-1992;   92US-00857224.
XX
PA   (BENN/) BENNER S A.
XX
PI   Benner SA;
XX
DR   WPI; 1999-570766/48.
XX
PT   Predicting the folded structure of proteins.
XX
PS   Disclosure; Col 253-256; 113pp; English.
XX
CC   Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC   predicting the folded structure of proteins, by aligning sequences of
CC   homologous proteins and using patterns of evolutionarily conserved and
CC   varied sequences to assign positions. Positions in the alignment are
CC   assigned to the surface or inside of the folded structure, active sites,
CC   and parsing segments. Secondary structural units are assigned by
CC   identifying periodicity in the assignments, and assembled into globular
CC   form using distance constraints imposed by disulfide bridges, active site
CC   assignments and co-variation analysis. The predicted secondary structures
CC   are useful for identifying antigenic sites on a protein molecule, as
CC   guides for site directed mutagenesis studies, and for understanding the
CC   interaction of a protein with other molecules
XX
SQ   Sequence 259 AA;

  Query Match             100.0%;  Score 51;  DB 2;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 0.63;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        246 DYLRSVLEDF 255


RESULT 12
ADR88385
ID   ADR88385 standard; protein; 263 AA.
XX
AC   ADR88385;
XX
DT   18-NOV-2004  (first entry)
XX
DE   LCK tyrosine kinase protein.
XX
KW   Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW   G-protein coupled receptor; methyl transferase; ligase;
KW   LCK tyrosine kinase; enzyme.
XX
OS   Unidentified.
XX
PN   US2004171062-A1.
XX
PD   02-SEP-2004.
XX
PF   28-FEB-2003; 2003US-00377268.
XX
PR   28-FEB-2002; 2002US-0360651P.
PR   16-SEP-2002; 2002US-0411398P.
PR   20-SEP-2002; 2002US-0412341P.
PR   02-JAN-2003; 2003US-0437929P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Hirth K,  Milburn MV;
XX
DR   WPI; 2004-642017/62.
XX
PT   Designing a ligand binding to a target molecule, comprises identifying as
PT   molecular scaffolds compounds binding to members of a molecular family,
PT   detecting orientation of scaffolds at a binding site of target, and
PT   synthesizing ligand.
XX
PS   Disclosure; SEQ ID NO 24; 186pp; English.
XX
CC   The present invention relates to a method of designing a ligand binding
CC   to a target molecule. The method involves identifying as molecular
CC   scaffolds compounds binding to members of a molecular family, detecting
CC   orientation of scaffolds at a binding site of target, and synthesising
CC   ligand. The invention is useful for designing drug products and for
CC   designing ligand binding to target molecules such as nuclear hormone
CC   receptors, TNF receptors, G-protein coupled receptors, methyl
CC   transferases, ligases, etc. The present sequence is the LCK tyrosine
CC   kinase protein. This sequence is used to illustrate the method of
CC   invention.
XX
SQ   Sequence 263 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 263;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        250 DYLRSVLEDF 259


RESULT 13
ABR56203
ID   ABR56203 standard; protein; 265 AA.
XX
AC   ABR56203;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).
XX
KW   Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW   Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW   mutant.
XX
OS   Homo sapiens.
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 128
FT                   /note= "Wild-type D substituted with N. This position is
FT                   364 in the full-length sequence (see ABR56202 for the
FT                   wild-type full length sequence"
FT   Modified-site   158
FT                   /note= "Phosphorylation site"
XX
PN   WO2003020880-A2.
XX
PD   13-MAR-2003.
XX
PF   02-AUG-2002; 2002WO-US024546.
XX
PR   03-AUG-2001; 2001US-0310051P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Borhani DW,  Calderwood D,  Dixon RW,  Hirst GC,  Hrnciar P,  Loew A;
PI   Leung A,  Ritter K;
XX
DR   WPI; 2003-300872/29.
XX
PT   New crystalline polypeptide comprising ligand binding domain or catalytic
PT   domain of Lck protein, for determining three-dimensional structure of
PT   catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS   Claim 12; Fig 2; 994pp; English.
XX
CC   The present invention relates to a crystalline polypeptide (I),
CC   comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC   protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC   in T-cells and plays an essential role in immune response. (I) is useful
CC   for identifying a compound which is an inhibitor of human Lck protein.
CC   The present sequence is a mutated fragment of the human Lck sequence,
CC   which approximately comprises the catalytic domain
XX
SQ   Sequence 265 AA;

  Query Match             100.0%;  Score 51;  DB 7;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 0.65;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        252 DYLRSVLEDF 261


RESULT 14
ABR56204
ID   ABR56204 standard; protein; 271 AA.
XX
AC   ABR56204;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N).
XX
KW   Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW   Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW   mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 134
FT                   /note= "Wild-type D substituted with N. This position is
FT                   364 in the full-length sequence (see ABR56202 for the
FT                   wild-type full length sequence"
FT   Modified-site   164
FT                   /note= "Phosphorylation site"
XX
PN   WO2003020880-A2.
XX
PD   13-MAR-2003.
XX
PF   02-AUG-2002; 2002WO-US024546.
XX
PR   03-AUG-2001; 2001US-0310051P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Borhani DW,  Calderwood D,  Dixon RW,  Hirst GC,  Hrnciar P,  Loew A;
PI   Leung A,  Ritter K;
XX
DR   WPI; 2003-300872/29.
XX
PT   New crystalline polypeptide comprising ligand binding domain or catalytic
PT   domain of Lck protein, for determining three-dimensional structure of
PT   catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS   Example 1; Fig 3; 994pp; English.
XX
CC   The present invention relates to a crystalline polypeptide (I),
CC   comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC   protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC   in T-cells and plays an essential role in immune response. (I) is useful
CC   for identifying a compound which is an inhibitor of human Lck protein.
CC   The present sequence is a mutated fragment of the human Lck sequence,
CC   which approximately comprises the catalytic domain
XX
SQ   Sequence 271 AA;

  Query Match             100.0%;  Score 51;  DB 7;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 0.67;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        258 DYLRSVLEDF 267


RESULT 15
ADY85449
ID   ADY85449 standard; protein; 279 AA.
XX
AC   ADY85449;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Catalytic domain of PIM kinase-like protein LCK.
XX
KW   Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW   neoplasm; inflammation; antiinflammatory.
XX
OS   Unidentified.
XX
PN   WO2005028624-A2.
XX
PD   31-MAR-2005.
XX
PF   15-SEP-2004; 2004WO-US030360.
XX
PR   15-SEP-2003; 2003US-0503277P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Artis DR,  Bremer RE,  Gillette SJ,  Hurt CR,  Ibrahim PL;
PI   Zuckerman RL;
XX
DR   WPI; 2005-273155/28.
XX
PT   New scaffold library used for identifying and developing ligands for
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PT   protein kinases and treating kinase associated disorders e.g. cancer,
PT   comprises set of compounds comprising N-heterocyclic compounds.
XX
PS   Disclosure; Page 170-174; 236pp; English.
XX
CC   The invention relates to a new kinase scaffold library comprises at least
CC   1 set of compounds, each set comprising at least 1 N-heterocyclic
CC   compound of formulae (I)-(VII) given in the specification. Also included
CC   are a system for fitting compounds in binding sites of protein kinases
CC   (comprising an electronic kinase scaffold, and a scaffold library
CC   comprising at least 1 collection of electronic representations of (I)-
CC   (VII), where the scaffold library is embedded in a computer device and
CC   the electronic representations of the compounds can be selectively
CC   retrieved and functionally connected with computer software adapted to
CC   fit electronic representations of compounds in an electronic
CC   representation of a binding site of a kinase), obtaining improved ligands
CC   binding to a protein kinase (which comprises determining if a derivative
CC   of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC   than (I)-(VII)), developing ligands specific for a particular kinase
CC   (which comprises determining if a derivative of (I)-(VII) that binds to
CC   kinases has greater for specificity for the particular kinase than (I)-
CC   (VII), developing ligands binding to a kinase (which comprises
CC   determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC   in co-crystals with the kinase, identifying chemical structures of the
CC   scaffolds, that, when modified, change the binding affinity and/or
CC   specificity between the scaffold and kinase and synthesizing a ligand in
CC   which at least 1 chemical structure of the scaffold is modified),
CC   developing ligands with increased specificity on a kinase (which
CC   comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC   increased specificity on the kinase), identifying a ligand binding to a
CC   kinase (which comprises determining if a derivative compound including a
CC   core structure (I)-(VII) binds to the kinase with changed binding
CC   affinity and/or specificity), a co-crystal of a kinase and a binding
CC   compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC   identifying potential kinase binding compounds (which comprises fitting
CC   electronic representations of (I)-(VII) in an electronic representation
CC   of a kinase binding site), attaching a kinase binding compound to an
CC   attachment component (which comprises identifying energetically allowed
CC   sites for attachment of the component on a kinase binding compound (I)-
CC   (VII) and attaching the compound or derivative to the attachment
CC   component at the allowed site), modified compounds (comprising (I)-(VIII)
CC   with an attached linker group, and developing a ligand for a kinase
CC   comprising conserved residues matching at least on of Pim-1 residues 49,
CC   52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC   to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC   vascular endothelial growth factor receptor, endothelial growth factor
CC   receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC   library is used for identifying and developing ligands binding to
CC   kinases, for modulating kinase activity and for treating disease
CC   condition associated with abnormal kinase activity e.g. cancer,
CC   inflammatory disease. The method identifies improved ligands binding to a
CC   kinase resulting in ligands having high affinity and specificity towards
CC   kinase. The co-crystals of kinase and the binding compound are of
CC   sufficient size and quality to allow structural determination of at least
CC   2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC   kinase. NOTE: It is not clear whether the sequence as presented
CC   represents a continuous amino acid sequence.
XX
SQ   Sequence 279 AA;

  Query Match             100.0%;  Score 51;  DB 9;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 0.69;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        258 DYLRSVLEDF 267


RESULT 16
AAY76750
ID   AAY76750 standard; protein; 346 AA.
XX
AC   AAY76750;
XX
DT   17-APR-2000  (first entry)
XX
DE   Human protein kinase homologue, PKH-3.
XX
KW   Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS;
KW   autoimmune disorder; inflammatory disorder; reproductive defect; asthma;
KW   diabetes mellitus; infertility; ovulatory defect; endometriosis;
KW   polycystic ovary syndrome.
XX
OS   Homo sapiens.
XX
PN   US6013455-A.
XX
PD   11-JAN-2000.
XX
PF   15-OCT-1998;   98US-00173581.
XX
PR   15-OCT-1998;   98US-00173581.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Hillman JL,  Yue H,  Yang YT,  Corley NC,  Gorgone GA,  Azimzai Y;
PI   Lu DAM,  Bandman O,  Guegler KJ;
XX
DR   WPI; 2000-136321/12.
DR   N-PSDB; AAZ86794.
XX
PT   Nucleic acids encoding a human protein kinase homolog useful for
PT   preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT   disorders and reproductive defects.
XX
PS   Claim 1; Col 47-50; 38pp; English.
XX
CC   This sequence represents a human protein kinase homolog (PKH) of the
CC   invention. The PKH sequences may be used in the prevention, treatment and
CC   diagnosis of diseases associated with inappropriate PKH expression such
CC   as cancers, autoimmune/inflammatory disorders and reproductive defects.
CC   They may be used to treat disorders associated with decreased PKH
CC   expression such as cancers (e.g. lymphoma, melanoma and cancers of the
CC   breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS,
CC   asthma and diabetes mellitus), and reproductive defects (e.g.
CC   infertility, ovulatory defects, endometriosis and polycystic ovary
CC   syndrome). The DNA may be administered to treat diseases by rectifying
CC   mutations or deletions in a patient's genome that affect the activity of
CC   PKH by expressing inactive proteins or to supplement the patients own
CC   production of PKH polypeptides. Additionally, the DNA may be used to
CC   produce PKH, according to standard recombinant DNA methodology, by
CC   inserting the nucleic acids into a host cell and culturing the cell to
CC   express the protein. Conversely, antisense nucleic acid molecules may be
CC   administered to down regulate PKH expression by binding with the cells
CC   own PKH genes and preventing their expression. The DNA, and antisense
CC   sequences may also be used as DNA probes in diagnostic assays to detect
CC   and quantitate the presence of similar nucleic acid sequences in samples,
CC   and hence which patients may be in need of restorative therapy. They may
CC   also be used to study the expression and function of PKH polypeptides and
CC   their role in metabolism. The PKH polypeptides may be used as antigens in
CC   the production of antibodies against PKH and in assays to identify
CC   modulators (agonists and antagonists) of PKH expression and activity. The
CC   anti-PKH antibodies and PKH antagonists may also be used to down regulate
CC   PKH expression and activity. The anti-PKH antibodies may also be used as
CC   diagnostic agents for detecting the presence of PKH polypeptides in
CC   samples
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 51;  DB 3;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
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```

```
Db        325 DYLRSVLEDF 334

RESULT 17
AAE06208
ID   AAE06208 standard; protein; 346 AA.
XX
AC   AAE06208;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human protein kinase homolog-3 (PKH-3).
XX
KW   Human; protein kinase homolog-3; PKH-3; cytostatic; protein therapy;
KW   vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma;
KW   Acquired Immune deficiency Syndrome; AIDS; melanoma; cancer; bone; liver;
KW   breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia;
KW   Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder;
KW   reproductive disorder; polycystic ovary syndrome; asthma.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          125. .333
FT                   /note= "Signature sequence"
XX
PN   US6264947-B1.
XX
PD   24-JUL-2001.
XX
PF   20-OCT-1999;   99US-00420915.
XX
PR   15-OCT-1998;   98US-00173581.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Bandman O,  Tang YT,  Hillman JL,  Yue H,  Guegler KJ,  Corley NC;
PI   Gorgone GA,  Azimzai Y,  Lu DAM;
XX
DR   WPI; 2001-450728/48.
DR   N-PSDB; AAD11845.
XX
PT   Human protein kinase proteins and homologs, useful for preventing,
PT   diagnosing and treating cancers, autoimmune/inflammatory disorders and
PT   reproductive disorders.
XX
PS   Claim 1; Col 47-50; 38pp; English.
XX
CC   The present sequence is human protein kinase homolog-3 (PKH-3). Human
CC   protein kinase homologs (PKH) and their cDNA molecules are used in the
CC   prevention, diagnosis and treatment of diseases associated with increased
CC   or decreased expression of PKH. Examples of such disorders include,
CC   cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer),
CC   autoimmune/inflammatory disorders (e.g. Acquired Immune deficiency
CC   Syndrome (AIDS), anaemia, asthma, Crohn's disease and multiple sclerosis)
CC   and reproductive disorders (e.g. tubal disease, ectopic pregnancy and
CC   polycystic ovary syndrome). PKH, its catalytic or immunogenic fragment
CC   are used for screening libraries of compounds in any of the drug
CC   screening techniques. PKH nucleic acids are used to generate
CC   hybridisation probes useful in mapping the naturally occurring genomic
CC   sequences. PKH are also used as antigens in the production of antibodies
CC   against protein kinases (PK) and in assays to identify modulators of PK
CC   expression and activity. PKH is also used in protein therapy
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 51;  DB 4;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        325 DYLRSVLEDF 334

RESULT 18
ABB84435
ID   ABB84435 standard; protein; 346 AA.
XX
AC   ABB84435;
XX
DT   08-NOV-2002  (first entry)
XX
DE   Human protein kinase homologue from clone 507669.
XX
KW   Protein kinase homologue; PKH; cytostatic; immunosuppressive; antifungal;
KW   antiinflammatory; antiallergic; antiasthmatic; antianaemic; antidiabetic;
KW   antiarteriosclerotic; antithyroid; dermatological; nephrotropic; human;
KW   antigout; thyromimetic; nootropic; osteopathic; antiarthritic; allergy;
KW   antirheumatic; ophthalmological; antiulcer; antiviral; antibacterial;
KW   antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis;
KW   acquired immunodeficiency syndrome; AIDS; Addison's disease; amyloidosis;
KW   adult respiratory distress syndrome; anaemia; asthma; atherosclerosis;
KW   autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis;
KW   cholecystitis; contact dermatitis; Crohn's disease; atopic dermatitis;
KW   dermatomyositis; diabetes mellitus; emphysema; atrophic gastritis; gout;
KW   glomerulonephritis; Goodpasture's syndrome; Graves' disease; psoriasis;
KW   Hashimoto's thyroiditis; hypereosinophilia; irritable bowel syndrome;
KW   multiple sclerosis; myasthenia gravis; myocardial inflammation; uveitis;
KW   pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis;
KW   polymyositis; Reiter's syndrome; rheumatoid arthritis; scleroderma; SLE;
KW   Sjogren's syndrome; systemic lupus erythematosus; systemic sclerosis;
KW   thrombocytopenic purpura; ulcerative colitis; Werner syndrome; infection;
KW   haemodialysis; extracorporeal circulation; infertility; tubal disease;
KW   ovulatory defect; endometriosis; oestrous; menstrual cycle; gene therapy;
KW   uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme;
KW   ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   US2002081290-A1.
XX
PD   27-JUN-2002.
XX
PF   30-MAY-2001; 2001US-00870962.
XX
PR   15-OCT-1998;   98US-00173581.
PR   20-OCT-1999;   99US-00420915.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Bandman O,  Tang YT,  Hillman JL,  Yue H,  Guegler KJ,  Corley NC;
PI   Gorgone GA,  Azimzai Y,  Lu DAM;
XX
DR   WPI; 2002-655433/70.
DR   N-PSDB; ABQ76288.
XX
PT   Nucleic acids encoding a human protein kinase homolog useful for
PT   preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT   disorders and reproductive defects.
XX
PS   Claim 47; Page 27; 43pp; English.
XX
CC   This invention describes a novel protein kinase homologue (PKH)
CC   polypeptides which have cytostatic, immunosuppressive, antiinflammatory,
CC   antiallergic, antiasthmatic, antianaemic, antiarteriosclerotic,
CC   antithyroid, dermatological, antidiabetic, nephrotropic, antigout,
CC   thyromimetic, nootropic, osteopathic, antiarthritic, antirheumatic,
CC   ophthalmological, antiulcer, antiviral, antibacterial, antifungal,
CC   antiprotozoal, antiparasitic and antihelmintic activity. The polypeptide
CC   is used for treating a disease or condition associated with decreased
CC   expression of functional PKH. The polypeptide is used to screen for
CC   agonists and antagonists of PKH which can also be used in disease
CC   treatment. The polypeptide and polynucleotide are used for treating
CC   acquired immunodeficiency syndrome (AIDS), Addison's disease, adult
```

```
CC   respiratory distress syndrome, allergies, ankylosing spondylitis,
CC   amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer,
CC   contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis,
CC   diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis,
CC   Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis,
CC   hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
CC   myasthenia gravis, myocardial or pericardial inflammation,
CC   osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC   Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC   systemic lupus erythematosus (SLE), systemic sclerosis, thrombocytopenic
CC   purpura, ulcerative colitis, uveitis, Werner syndrome, complications of
CC   cancer, haemodialysis, and extracorporeal circulation, viral, bacterial,
CC   fungal, parasitic, protozoal, and helminthic infections, infertility,
CC   including tubal disease, ovulatory defects, and endometriosis,
CC   disruptions of the oestrous cycle, disruptions of the menstrual cycle,
CC   polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial
CC   and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic
CC   pregnancies, and teratogenesis. The polypeptides of the invention can be
CC   used for gene therapy. This sequence represents a PKH from clone ID
CC   507669 isolated from TMLR3DT02, a library constructed using RNA isolated
CC   from non-adherent peripheral blood mononuclear cells collected from a
CC   pool of male and female donors
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 51;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        325 DYLRSVLEDF 334


RESULT 19
ABM82980
ID   ABM82980 standard; protein; 355 AA.
XX
AC   ABM82980;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:3229.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN41632.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 355 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 0.88;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        334 DYLRSVLEDF 343


RESULT 20
AAR14201
ID   AAR14201 standard; protein; 417 AA.
XX
AC   AAR14201;
XX
DT   13-DEC-1991  (first entry)
XX
DE   (Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
XX
KW   Multi-cloning site.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .26
FT                   /note= "beta-galactosidase fragment"
FT   Region          27. .417
FT                   /note= "lck gene polypeptide"
XX
PN   JP03201994-A.
XX
PD   03-SEP-1991.
XX
PF   28-DEC-1989;   89JP-00338268.
XX
PR   28-DEC-1989;   89JP-00338268.
XX
PA   (TOKU ) TOKUYAMA SODA KK.
XX
DR   WPI; 1991-300980/41.
DR   N-PSDB; AAQ14201.
XX
PT   Fused polypeptide - has amino acid sequence of beta-galactosidase with a
PT   LCK gene conjugated to the N-terminal via DNA having multi-cloning site.
XX
PS   Claim 1; Fig 4,2; 15pp; Japanese.
XX
CC   The sequence consists of the N-terminal amino acids of the beta-
```

CC galactosidase gene fused with the lck gene. It is produced by E.coli
CC transformed with a recombinant vector (see AAQ13983). It is useful for
CC producing an antibody specifically immunoreactive with only a lck gene-
CC derived polypeptide in T cells. The antibody may recognise lck gene-
CC derived polypeptides in human cells
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 51; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10
||||||||||
Db 396 DYLRSVLEDF 405

RESULT 21
ADC99048
ID ADC99048 standard; protein; 458 AA.
XX
AC ADC99048;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human KPP protein - SEQ ID 1.
XX
KW anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
KW cancer; developmental; mental retardation; neurological;
KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; human; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003033680-A2.
XX
PD 24-APR-2003.
XX
PF 17-OCT-2002; 2002WO-US033723.
XX
PR 19-OCT-2001; 2001US-0345474P.
PR 02-NOV-2001; 2001US-0343910P.
PR 13-NOV-2001; 2001US-0333098P.
PR 16-NOV-2001; 2001US-0332424P.
PR 30-NOV-2001; 2001US-0334288P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
PI Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
PI Zebarjadian Y;
XX
DR WPI; 2003-403214/38.
DR N-PSDB; ADC99100.
XX
PT New human kinases and phosphatases and polynucleotides, useful for
PT diagnosing, treating or preventing autoimmune or inflammatory disorders
PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT cancer or hepatitis.
XX
PS Claim 1; SEQ ID NO 1; 424pp; English.
XX
CC The invention relates to a novel isolated polypeptide which is a human
CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
CC agonists and antagonists are useful for diagnosing, treating or
CC preventing cell proliferative disorders such as atherosclerosis,
CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
CC retardation, neurological disorders including Alzheimer's disease and
CC Parkinson's disease, autoimmune and inflammatory disorders such as
CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,
CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the
CC polynucleotides encoding KPP may be useful for creating transgenic
CC animals to model human disease, as well as during gene therapy
CC procedures. The current sequence is that of the human KPP protein of the
CC invention.
XX
SQ Sequence 458 AA;

Query Match 100.0%; Score 51; DB 7; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10
||||||||||
Db 437 DYLRSVLEDF 446

RESULT 22
AAE21689
ID AAE21689 standard; protein; 502 AA.
XX
AC AAE21689;
XX
DT 29-AUG-2003 (revised)
DT 16-JUL-2002 (first entry)
XX
DE Fugu rubripes lymphocyte kinase (LCK) protein.
XX
KW T-lymphocyte modulator; autoimmune disorder; graft rejection;
KW graft-versus-host disease; viral infection; lymphocyte kinase; LCK.
XX
OS Takifugu rubripes.
XX
PN WO200218619-A2.
XX
PD 07-MAR-2002.
XX
PF 16-AUG-2001; 2001WO-IL000765.
XX
PR 01-SEP-2000; 2000US-0229326P.
XX
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA (EHRL/) EHRLICH G.
XX
PI Brenner S, Venkatesh B, Tan YH;
XX
DR WPI; 2002-329781/36.
DR N-PSDB; AAD34173.
XX
PT New nucleic acids, useful for regulating T-cell mediated immune
PT responses, e.g., suppressing T-lymphocytes in subjects with autoimmune
PT disorders, or enhancement in those with viral infections, comprises novel
PT T-cell active promoters.
XX
PS Example 2; Page 55-57; 67pp; English.
XX
CC The invention relates to an isolated nucleic acid which includes a
CC promoter sequence being transcriptionally functional in a T-lymphocyte
CC undergoing activation and transcriptionally less functional in the T-
CC lymphocyte prior to the activation. The nucleic acid is useful for
CC regulating T-cell mediated immune responses in mammals. Nucleic acid
CC molecules of the invention may be used to suppress or eliminate T-
CC lymphocytes undergoing activation to suppress T-lymphocyte mediated
CC immune response in individuals suffering from immune disorders, e.g.

```
CC   autoimmune disorders such as graft rejection or graft-versus-host
CC   disease. They may also be used to enhance T-lymphocyte mediated immune
CC   response in individual suffering from, e.g. viral infection. The present
CC   sequence is Fugu rubripes lymphocyte kinase (LCK) protein. (Updated on 29
CC   -AUG-2003 to standardise OS field)
XX
SQ   Sequence 502 AA;

  Query Match             100.0%;  Score 51;  DB 5;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        483 DYLRSVLEDF 492


RESULT 23
AAB37700
ID   AAB37700 standard; protein; 508 AA.
XX
AC   AAB37700;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human lymphocyte kinase.
XX
KW   Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
XX
OS   Homo sapiens.
XX
PN   WO200070030-A1.
XX
PD   23-NOV-2000.
XX
PF   19-MAY-2000; 2000WO-US013881.
XX
PR   19-MAY-1999;   99US-0134965P.
XX
PA   (KINE-) KINETIX PHARM INC.
XX
PI   Zhu X;
XX
DR   WPI; 2000-687708/67.
XX
PT   Crystal of a protein-ligand complex for identifying kinase inhibitors,
PT   comprises a truncated lymphocyte kinase and a ligand, and diffracts X-
PT   rays to determine atomic coordinates at a resolution greater than 5
PT   angstroms.
XX
PS   Claim 1; Page 434-5; 438pp; English.
XX
CC   The present invention relates to a crystal of a protein-ligand complex
CC   comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal
CC   diffracts X-rays so that the atomic coordinates of the protein-ligand
CC   complex can be determined to a resolution of greater than 5.0 Angstroms.
CC   The truncated lck used in the present invention comprises the globular
CC   core of the corresponding full-length lck. The present sequence is the
CC   full-length human lck protein. The crystal of the present invention may
CC   be used to identify kinase inhibitors in screening assays, in drug
CC   screening and drug design processes, to design, select or test inhibitors
CC   of kinase enzymes, where the inhibitors are used as therapeutics for the
CC   treatment and modulation of diseases, disease symptoms or the effect of
CC   other physiological events mediated by kinases, having one or more kinase
CC   enzymes involved in their pathology
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 51;  DB 3;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        487 DYLRSVLEDF 496


RESULT 24
ADE58802
ID   ADE58802 standard; protein; 508 AA.
XX
AC   ADE58802;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06239, SEQ ID NO 4689.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 508 AA;
```

```
  Query Match             100.0%;  Score 51;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        487 DYLRSVLEDF 496


RESULT 25
ADE58799
ID   ADE58799 standard; protein; 508 AA.
XX
AC   ADE58799;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06239, SEQ ID NO 4686.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 51;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        487 DYLRSVLEDF 496


RESULT 26
ADF45072
ID   ADF45072 standard; protein; 508 AA.
XX
AC   ADF45072;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human kinase LCK.
XX
KW   Human; protein kinase; enzyme; inhibitor; LCK.
XX
OS   Homo sapiens.
XX
PN   WO2003081210-A2.
XX
PD   02-OCT-2003.
XX
PF   20-MAR-2003; 2003WO-US008725.
XX
PR   21-MAR-2002; 2002US-0366892P.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescott JC,  Braisted A;
XX
DR   WPI; 2003-865136/80.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase (T) comprises contacting the conformation modified (T) which
PT   contains reactive group at binding site, with ligands and detecting
PT   kinase-ligand conjugate formation.
XX
PS   Disclosure; SEQ ID NO 41; 260pp; English.
XX
CC   The present invention relates to a method for identifying a ligand (L),
CC   which binds to an inactive conformation of target protein kinase (T). The
CC   method involves contacting inactive conformation of (T), which contains
CC   or is modified to contain a reactive group at or near a binding site of
CC   interest, with one or more ligand candidates capable of covalently
CC   bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC   The method is useful for identifying protein kinase inhibitors that
CC   preferentially bind to inactive conformation of a target protein kinase.
CC   The present sequence is a protein kinase which may be modified via an
CC   amino acid substitution, for use in the method of the invention.
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 51;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        487 DYLRSVLEDF 496


RESULT 27
ADL34479
```

```
ID   ADL34479 standard; peptide; 508 AA.
XX
AC   ADL34479;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human lymphocyte kinase (Lck) globular core.
XX
KW   cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;
KW   fungicide; nootropic; neuroprotective; kinase inhibitor; crystal;
KW   protein-ligand complex; lymphocyte kinase; Lck; Lck ligand;
KW   kinase inhibitor; therapeutic; kinase-mediated physiological event;
KW   cancer; autoimmunological; metabolic; inflammatory; infection;
KW   central nervous system degenerative disease; transplant rejection; human;
KW   globular core; protein co-ordinate data.
XX
OS   Homo sapiens.
XX
PN   US6589758-B1.
XX
PD   08-JUL-2003.
XX
PF   21-MAY-2001; 2001US-00862154.
XX
PR   19-MAY-2000; 2000US-0205510P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zhu X;
XX
DR   WPI; 2003-810380/76.
XX
PT   Crystal of protein-ligand complex useful for identifying an inhibitor of
PT   lymphocyte kinase (Lck), comprises truncated Lck and a ligand.
XX
PS   Claim 1; SEQ ID NO 1; 295pp; English.
XX
CC   The invention describes a crystal (I) of a protein-ligand complex (C)
CC   comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I)
CC   effectively diffracts X-rays for determination of atomic coordinates of
CC   (C) to a resolution of greater than 5.0 angstroms, and truncated Lck
CC   comprises a sequence (S1) of residues 225-508 of a 508 amino acid
CC   sequence, given in specification and retains the globular core of full-
CC   length Lck. (I) is useful in an inhibitor screening assay and to
CC   identify, design, select, and evaluate potential inhibitors of kinases
CC   that would be useful as therapeutics for diseases or symptoms of diseases
CC   that are associated with kinase-mediated physiological events. The
CC   inhibitors identified by the methods may also be useful for inhibition of
CC   kinase activity of one or more enzymes. The inhibitors are also useful
CC   for inhibiting the biological activity of any enzyme comprising greater
CC   than 90%, alternatively greater than 85%, or alternatively greater than
CC   70% sequence homology with a kinase sequence. The inhibitors are useful
CC   for inhibiting the biological activity of any enzyme that binds ATP and
CC   thus for treating disease or disease symptoms mediated by any enzyme that
CC   binds ATP. The inhibitors are useful in inhibiting kinase activity and
CC   are useful in treating kinase-mediated disease or disease symptoms in a
CC   mammal, particularly a human e.g., cancer, autoimmunological, metabolic,
CC   inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central
CC   nervous system degenerative disease etc. The inhibitors are useful in
CC   treating or preventing diseases, including, transplant rejection etc.
CC   This is the amino acid sequence of a human lymphocyte kinase (Lck)
CC   polypeptide comprising the Lck globular core.
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 51;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        487 DYLRSVLEDF 496
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RESULT 28
ADS88148
ID   ADS88148 standard; protein; 508 AA.
XX
AC   ADS88148;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
XX
KW   protein complex; tumour necrosis factor-alpha signalling pathway;
KW   TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW   inflammatory bowel disease; infectious disease; septic shock;
KW   bacterial infection; neurological disease; stroke-induced inflammation;
KW   neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW   antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO2004035783-A2.
XX
PD   29-APR-2004.
XX
PF   24-SEP-2003; 2003WO-EP050655.
XX
PR   26-SEP-2002; 2002EP-00021809.
PR   10-FEB-2003; 2003EP-00100274.
XX
PA   (CELL-) CELLZOME AG.
XX
PI   Bouwmeester T,  Huhse B,  Bauch A,  Ruffner H,  Bauer A,  Kuester B;
PI   Superti-Furga G,  Kruse U;
XX
DR   WPI; 2004-348460/32.
XX
PT   New protein complex comprising at least one first and second protein of
PT   the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
PT   diagnosing or treating inflammation, neurological diseases, infectious
PT   diseases or cancer.
XX
PS   Example; SEQ ID NO 3; 1980pp; English.
XX
CC   This invention relates to novel protein complexes of the tumour necrosis
CC   factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC   methods for preparing these complexes comprising at least two component
CC   proteins, as well as screening methods to identify modulators of the
CC   pathway, which include antibodies, agonists and antagonists thereof. The
CC   present invention describes a protein complex and kit that are useful for
CC   diagnosing, prognosing or treating chronic inflammatory diseases such as
CC   rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC   such as septic shock and bacterial infections; neurological diseases such
CC   as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC   cancer. Accordingly, these complexes can be used for the development of
CC   pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC   antirheumatic, cytostatic and antibacterial activities and can be used
CC   for gene therapy purposes. In particular, the invention further provides
CC   siRNA-oligonucleotides useful for inhibiting protein expression for in
CC   vitro or cell culture assays. This polypeptide is a human protein that
CC   can be used in combination with other proteins provided in the
CC   specification to form novel complexes of the TNF-alpha signalling pathway
CC   of the invention.
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        487 DYLRSVLEDF 496
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RESULT 29
AAY49420
ID   AAY49420 standard; protein; 509 AA.
XX
AC   AAY49420;
XX
DT   13-MAR-2000  (first entry)
XX
DE   PKA substrate, Src-family protein.
XX
KW   Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW   kinase substrate; immunosuppressive disorder; proliferative disease;
KW   HIV infection; AIDS; immunodeficiency; autoimmune disease;
KW   systemic lupus erythematosus; Src-family.
XX
OS   Homo sapiens.
XX
PN   WO9962315-A2.
XX
PD   02-DEC-1999.
XX
PF   27-MAY-1999;   99WO-GB001680.
XX
PR   27-MAY-1998;   98NO-00002419.
PR   30-DEC-1998;   98US-0114240P.
XX
PA   (LAUR-) LAURAS AS.
PA   (JONE/) JONES E L.
XX
PI   Hansson V,  Levy FO,  Mustelin T,  Skalhegg BS,  Sundvold V;
PI   Tasken K,  Vang T,  Altman A,  Munshi A;
XX
DR   WPI; 2000-086801/07.
DR   N-PSDB; AAZ46491.
XX
PT   Altering the activity of protein kinase signaling pathways, used for
PT   treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,
PT   e.g. cancers or autoimmune diseases.
XX
PS   Claim 23; Page 95-96; 111pp; English.
XX
CC   The invention provides a novel method of altering the activity of the
CC   protein kinase A (PKA) signaling pathway in a cell that comprises
CC   altering the extent of phosphorylation of one or more PKA substrates, or
CC   kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC   compositions containing a nucleic acid molecule that encodes a PKA
CC   substrate, or fragment, precursor or functionally equivalent variant,
CC   where the sequence is modified to alter its susceptibility to
CC   phosphorylation by PKA can be used for treating a disorder exhibiting
CC   abnormal PKA signaling activity, immunosuppressive disorders or
CC   proliferative diseases. They can be used for treating e.g. HIV infection,
CC   AIDS, common variable immunodeficiency or cancers. Conditions in which
CC   upregulation of the PKA pathway is required, such as autoimmune disease,
CC   e.g. systemic lupus erythematosus, may also be treated. The present
CC   sequence represents a PKA substrate, wherein the substrate is in the Src-
CC   family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl,
CC   Fyk, Src-1 or Src-2
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 51;  DB 3;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        488 DYLRSVLEDF 497


RESULT 30
ABR58699
ID   ABR58699 standard; protein; 509 AA.
XX
AC   ABR58699;
XX
DT   09-JUL-2003  (first entry)
XX
DE   Human cancer related protein SEQ ID NO:356.
XX
KW   Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW   heart disease; atherosclerosis; endometriosis.
XX
OS   Homo sapiens.
XX
PN   WO2003025138-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-US029560.
XX
PR   17-SEP-2001; 2001US-0323469P.
PR   20-SEP-2001; 2001US-0323887P.
PR   13-NOV-2001; 2001US-0350666P.
PR   08-FEB-2002; 2002US-0355145P.
PR   08-FEB-2002; 2002US-0355257P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Gish KC,  Hevezi PA,  Mack DH,  Wilson KE;
PI   Zlotnik A;
XX
DR   WPI; 2003-354600/33.
DR   N-PSDB; ACC72850.
XX
PT   New genes that are up-regulated or down-regulated in cancers, useful as
PT   markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT   therapeutic targets for screening drugs for treating these diseases.
XX
PS   Claim 12; Page 762; 767pp; English.
XX
CC   The present invention describes an isolated nucleic acid molecule, which
CC   comprises the sequence of any of the genes that are up-regulated or down-
CC   regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC   acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC   related gene nucleotide sequences which encode the proteins given in
CC   ABR58521 to ABR58709. Also described: (1) determining the presence or
CC   absence of a pathological cell in a patient; (2) an expression vector
CC   comprising a nucleic acid molecule described above; (3) a host cell
CC   comprising the vector; (4) an isolated polypeptide, which is encoded by
CC   the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC   of (4); (6) specifically targeting a compound to a pathological cell in a
CC   patient by administering to the patient the antibody above; and (7) a
CC   drug screening assay. The nucleic acid is useful as diagnostic markers or
CC   therapeutic targets. In particular, the nucleic acid is useful for
CC   diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC   bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC   pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC   atherosclerosis and endometriosis. The nucleic acid is also useful in
CC   drug screening, particularly for identifying agents for treating these
CC   pathologies
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        488 DYLRSVLEDF 497


Search completed: June 29, 2006, 09:13:12
Job time : 98.5904 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 105.831 Seconds
(without alignments)
78.664 Million cell updates/sec

Title: US-10-062-257A-1
Perfect score: 45
Sequence: 1 TFDYLRSVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	368	2	Q3TLX4_MOUSE	Q3tlx4 mus musculu
2	45	100.0	379	2	Q4FZR6_RAT	Q4fzr6 rattus norv
3	45	100.0	502	2	Q8QGJ9_FUGRU	Q8qgj9 fugu rubrip
4	45	100.0	508	1	LCK_AOTNA	Q5pxs1 aotus nancy
5	45	100.0	508	1	LCK_HUMAN	P06239 homo sapien
6	45	100.0	508	1	LCK_MOUSE	P06240 mus musculu
7	45	100.0	508	1	LCK_SAISC	Q95kr7 saimiri sci
8	45	100.0	509	2	Q7RTZ3_HUMAN	Q7rtz3 homo sapien
9	45	100.0	509	2	Q95M32_9PRIM	Q95m32 hylobates s
10	45	100.0	509	2	Q3ZCM0_BOVIN	Q3zcm0 bos taurus
11	45	100.0	516	2	Q573B4_HUMAN	Q573b4 homo sapien
12	42	93.3	249	2	Q9U8V6_EPTBU	Q9u8v6 eptatretus
13	41	91.1	318	2	Q2UQK7_ASPOR	Q2uqk7 aspergillus
14	41	91.1	466	2	Q4RNX3_TETNG	Q4rnx3 tetraodon n
15	41	91.1	488	2	O13064_XENLA	O13064 xenopus lae
16	41	91.1	491	2	Q3U6Q5_MOUSE	Q3u6q5 mus musculu
17	41	91.1	491	2	Q8CEI0_MOUSE	Q8cei0 mus musculu
18	41	91.1	492	2	Q5ZMB9_CHICK	Q5zmb9 gallus gall
19	41	91.1	511	1	LYN_HUMAN	P07948 homo sapien
20	41	91.1	511	1	LYN_MOUSE	P25911 mus musculu
21	41	91.1	511	1	LYN_RAT	Q07014 rattus norv
22	41	91.1	512	2	Q3TCS3_MOUSE	Q3tcs3 m nod-deriv
23	41	91.1	582	2	Q6NUK7_HUMAN	Q6nuk7 homo sapien
24	39	86.7	510	2	Q66I04_BRARE	Q66i04 brachydanio
25	38	84.4	605	2	Q4X0L1_ASPFU	Q4x0l1 aspergillus
26	38	84.4	606	2	Q5AZN3_EMENI	Q5azn3 aspergillus
27	37	82.2	98	2	Q86TW9_HUMAN	Q86tw9 homo sapien
28	37	82.2	267	2	Q5FWT4_RAT	Q5fwt4 rattus norv
29	37	82.2	379	2	Q8YMU7_ANASP	Q8ymu7 anabaena sp
30	37	82.2	381	2	Q3MBB4_ANAVT	Q3mbb4 anabaena va
31	37	82.2	499	2	Q8J1E4_LIPKO	Q8j1e4 lipomyces k
32	37	82.2	502	2	Q9DDK6_SALSA	Q9ddk6 salmo salar
33	37	82.2	503	2	Q6TPQ4_BRARE	Q6tpq4 brachydanio
34	37	82.2	509	1	STK_HYDAT	P17713 hydra atten
35	37	82.2	519	2	Q80Y28_MOUSE	Q80y28 mus musculu
36	37	82.2	589	2	Q5NQ10_ZYMMO	Q5nq10 zymomonas m
37	37	82.2	606	1	ABCD4_HUMAN	O14678 homo sapien
38	37	82.2	606	1	ABCD4_MOUSE	O89016 mus musculu
39	37	82.2	606	2	Q6IAQ0_HUMAN	Q6iaq0 homo sapien
40	37	82.2	606	2	Q96E75_HUMAN	Q96e75 homo sapien
41	37	82.2	789	1	KSB_CUCMA	Q39548 cucurbita m
42	36	80.0	292	1	DCNL4_MOUSE	Q8cca0 mus musculu
43	36	80.0	292	2	Q2YDW5_MOUSE	Q2ydw5 mus musculu
44	36	80.0	306	2	Q8C5X2_MOUSE	Q8c5x2 mus musculu
45	36	80.0	308	1	LIPA_CHLMU	Q9pji2 chlamydia m
46	36	80.0	311	1	LIPA_CHLTR	O84562 chlamydia t
47	36	80.0	311	2	Q3KLD9_CHLTA	Q3kld9 chlamydia t
48	36	80.0	457	2	Q40NJ1_DESAC	Q40nj1 desulfuromo
49	36	80.0	496	2	O93411_XENLA	O93411 xenopus lae
50	36	80.0	507	1	LCK_CHICK	P42683 gallus gall
51	36	80.0	2609	2	Q7SG70_NEUCR	Q7sg70 neurospora
52	36	80.0	2627	2	Q4IQE1_GIBZE	Q4iqe1 gibberella
53	36	80.0	2708	2	O15791_PLAFA	O15791 plasmodium
54	36	80.0	2729	2	Q8IBZ6_PLAF7	Q8ibz6 plasmodium
55	36	80.0	2742	2	O15801_PLAFA	O15801 plasmodium
56	36	80.0	2819	2	O15792_PLAFA	O15792 plasmodium
57	35	77.8	57	2	Q58LM5_9CAUD	Q58lm5 cyanophage
58	35	77.8	80	2	Q5BT64_SCHJA	Q5bt64 schistosoma
59	35	77.8	99	2	Q4XNK1_PLACH	Q4xnk1 plasmodium
60	35	77.8	114	2	Q4JB12_SULAC	Q4jb12 sulfolobus
61	35	77.8	151	2	Q5FFY4_EHRRG	Q5ffy4 ehrlichia r
62	35	77.8	151	2	Q5HAN1_EHRRW	Q5han1 ehrlichia r
63	35	77.8	157	2	Q61J95_CAEBR	Q61j95 caenorhabdi
64	35	77.8	187	2	Q9XVX5_CAEEL	Q9xvx5 caenorhabdi
65	35	77.8	191	2	Q86D99_CAEEL	Q86d99 caenorhabdi
66	35	77.8	196	2	Q5RHX5_BRARE	Q5rhx5 brachydanio
67	35	77.8	280	1	DCNL4_BRARE	Q5rhx6 brachydanio
68	35	77.8	281	2	Q4RKU7_TETNG	Q4rku7 tetraodon n
69	35	77.8	342	2	Q55XN5_CRYNE	Q55xn5 cryptococcu
70	35	77.8	342	2	Q5KMA1_CRYNE	Q5kma1 cryptococcu
71	35	77.8	347	2	Q7RLE3_PLAYO	Q7rle3 plasmodium
72	35	77.8	350	2	Q8IJ81_PLAF7	Q8ij81 plasmodium
73	35	77.8	502	1	HCK_RAT	P50545 rattus norv
74	35	77.8	503	1	HCK_MACFA	Q95m30 macaca fasc
75	35	77.8	503	2	Q3UD17_MOUSE	Q3ud17 m bone marr
76	35	77.8	503	2	Q6AYV7_RAT	Q6ayv7 rattus norv
77	35	77.8	511	2	Q4RL31_TETNG	Q4rl31 tetraodon n
78	35	77.8	523	1	HCK_MOUSE	P08103 mus musculu
79	35	77.8	525	1	HCK_HUMAN	P08631 homo sapien
80	35	77.8	541	2	Q76IP5_CANGA	Q76ip5 candida gla
81	35	77.8	570	2	Q504R5_HUMAN	Q504r5 homo sapien
82	35	77.8	580	2	Q2VPE2_HUMAN	Q2vpe2 homo sapien
83	35	77.8	660	2	Q44PN7_CHLLI	Q44pn7 chlorobium
84	35	77.8	785	2	Q9FRX5_CUCSA	Q9frx5 cucumis sat
85	35	77.8	877	1	SYA_RICPR	Q9zca4 rickettsia
86	34	75.6	80	2	Q54HC2_DICDI	Q54hc2 dictyosteli
87	34	75.6	169	2	Q5BYF7_SCHJA	Q5byf7 schistosoma
88	34	75.6	176	2	Q8FKP1_ECOL6	Q8fkp1 escherichia
89	34	75.6	202	2	Q4IMK6_GIBZE	Q4imk6 gibberella
90	34	75.6	211	2	Q06026_SOLCH	Q06026 solanum cha
91	34	75.6	222	2	Q836Y8_ENTFA	Q836y8 enterococcu
92	34	75.6	242	1	FLIG_SHIBO	P95715 shigella bo
93	34	75.6	250	2	Q31RT6_SYNP7	Q31rt6 synechococc
94	34	75.6	250	2	Q5N2H0_SYNP6	Q5n2h0 synechococc
95	34	75.6	282	2	Q2JYQ3_RHIET	Q2jyq3 rhizobium e
96	34	75.6	292	1	DCNL4_HUMAN	Q92564 homo sapien
97	34	75.6	297	2	Q4V4Y8_DROME	Q4v4y8 drosophila
98	34	75.6	326	2	Q5WYX0_LEGPL	Q5wyx0 legionella
99	34	75.6	326	2	Q5X7H4_LEGPA	Q5x7h4 legionella
100	34	75.6	326	2	Q5ZY00_LEGPH	Q5zy00 legionella

ALIGNMENTS

```
RESULT 1
Q3TLX4_MOUSE
ID   Q3TLX4_MOUSE   PRELIMINARY;   PRT;   368 AA.
AC   Q3TLX4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
DE   library, clone:G830026O06 product:lymphocyte protein tyrosine kinase,
DE   full insert sequence. (Fragment).
GN   Name=Lck;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AK166263; BAE38668.1; -; mRNA.
DR   MGI; MGI:96756; Lck.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   368 AA;  42018 MW;  7AB6AE53AF1A5059 CRC64;

  Query Match             100.0%;  Score 45;  DB 2;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        345 TFDYLRSVL 353


RESULT 2
Q4FZR6_RAT
ID   Q4FZR6_RAT     PRELIMINARY;   PRT;   379 AA.
AC   Q4FZR6;
DT   30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   30-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Lck_mapped protein (Fragment).
GN   Name=Lck_mapped;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC099218; AAH99218.1; -; mRNA.
DR   SMR; Q4FZR6; 2-379.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   379 AA;  43336 MW;  7CDEB573BAFB53AB CRC64;

  Query Match             100.0%;  Score 45;  DB 2;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
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Db        356 TFDYLRSVL 364
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RESULT 3
Q8QGJ9_FUGRU
ID   Q8QGJ9_FUGRU   PRELIMINARY;   PRT;   502 AA.
AC   Q8QGJ9;
DT   01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2002, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   Lymphocyte-specific c-src family protein tyrosine kinase.
GN   Name=lck;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21874085; PubMed=11867707; DOI=10.1073/pnas.032680599;
RA   Brenner S., Venkatesh B., Yap W.-H., Chou C.-F., Tay A.W.N.,
RA   Ponniah S., Wang Y., Tan Y.H.;
RT   "Conserved regulation of the lymphocyte-specific expression of lck in
RT   the Fugu and mammals.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:2936-2941(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AF411956; AAL89664.1; -; Genomic_DNA.
DR   HSSP; P06239; 1QPC.
DR   Ensembl; SINFRUG00000129447; Fugu rubripes.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   502 AA;  57477 MW;  A8C9EC2E774F79CD CRC64;

  Query Match             100.0%;  Score 45;  DB 2;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        481 TFDYLRSVL 489


RESULT 4
LCK_AOTNA
ID   LCK_AOTNA      STANDARD;      PRT;   508 AA.
AC   Q5PXS1;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 3.
DT   07-MAR-2006, entry version 13.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Perez-Quintero L.A., Vernot J.P.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY821852; AAV70114.2; -; mRNA.
DR   SMR; Q5PXS1; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
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DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088123.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID .       4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58041 MW;  8B61951BC192A3A4 CRC64;

  Query Match             100.0%;  Score 45;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        485 TFDYLRSVL 493


RESULT 5
LCK_HUMAN
ID   LCK_HUMAN      STANDARD;      PRT;   508 AA.
AC   P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 5.
DT   07-MAR-2006, entry version 87.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-
DE   specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87133831; PubMed=3493153;
RA   Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
RA   Mak T.W.;
RT   "A human T cell-specific cDNA clone (YT16) encodes a protein with
RT   extensive homology to a family of protein-tyrosine kinases.";
RL   Eur. J. Immunol. 16:1643-1646(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89123626; PubMed=3265417;
RA   Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
RA   Wilson C.B.;
RT   "Structure and expression of lck transcripts in human lymphoid
RT   cells.";
RL   J. Cell. Biochem. 38:117-126(1988).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
RA   Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
RA   Benarous R.;
RT   "Structure of the human lck gene: differences in genomic organisation
RT   within src-related genes affect only N-terminal exons.";
RL   Gene 84:105-113(1989).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;
RP   VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.
RC   TISSUE=Leukemia;
RX   MEDLINE=94187714; PubMed=8139546;
RA   Wright D.D., Sefton B.M., Kamps M.P.;
RT   "Oncogenic activation of the Lck protein accompanies translocation of
RT   the LCK gene in the human HSB2 T-cell leukemia.";
RL   Mol. Cell. Biol. 14:2429-2437(1994).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.
RC   TISSUE=Leukemic T-cell;
RX   MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
RA   Vogel L.B., Arthur R., Fujita D.J.;
RT   "An aberrant lck mRNA in two human T-cell lines.";
RL   Biochim. Biophys. Acta 1264:168-172(1995).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   Human chromosome 1 international sequencing consortium;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89096891; PubMed=2850479;
RA   Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT   "Structure of the murine lck gene and its rearrangement in a murine
RT   lymphoma cell line.";
RL   Mol. Cell. Biol. 8:3058-3064(1988).
RN   [9]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89313764; PubMed=2787474;
RA   Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA   Miyamoto N.G., Mak T.W.;
RT   "Structure of the two promoters of the human lck gene: differential
RT   accumulation of two classes of lck transcripts in T cells.";
RL   Mol. Cell. Biol. 9:2173-2180(1989).
RN   [10]
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RP   NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.
RC   TISSUE=Peripheral blood lymphocyte;
RX   MEDLINE=20462621; PubMed=11009097;
RX   DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
RA   Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S.,
RA   Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA   Baldari C.T.;
RT   "Defective recruitment and activation of ZAP-70 in common variable
RT   immunodeficiency patients with T cell defects.";
RL   Eur. J. Immunol. 30:2632-2638(2000).
RN   [11]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 367-508.
RX   MEDLINE=88217332; PubMed=2835736;
RA   Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RT   "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT   and other non-lymphoid human tumor cell lines.";
RL   Oncogene Res. 1:357-374(1987).
RN   [12]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 374-508.
RX   MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
RA   Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA   Linna T.J.;
RT   "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT   p56LSTRA.";
RL   Biochim. Biophys. Acta 888:286-295(1986).
RN   [13]
RP   PHOSPHORYLATION SITE TYR-504.
RX   MEDLINE=92347326; PubMed=1639064;
RA   Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA   Amrein K.E., Autero M., Burn P., Alitalo K.;
RT   "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT   down regulates its catalytic activity.";
RL   EMBO J. 11:2919-2924(1992).
RN   [14]
RP   INTERACTION WITH PI3K.
RX   MEDLINE=94067101; PubMed=7504174;
RA   Vogel L.B., Fujita D.J.;
RT   "The SH3 domain of p56lck is involved in binding to
RT   phosphatidylinositol 3'-kinase from T lymphocytes.";
RL   Mol. Cell. Biol. 13:7408-7417(1993).
RN   [15]
RP   INTERACTION WITH KHDRBS1.
RX   MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;
RA   Vogel L.B., Fujita D.J.;
RT   "p70 phosphorylation and binding to p56lck is an early event in
RT   interleukin-2-induced onset of cell cycle progression in T-
RT   lymphocytes.";
RL   J. Biol. Chem. 270:2506-2511(1995).
RN   [16]
RP   INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.
RX   PubMed=8618896;
RA   Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;
RT   "Phosphotyrosine-independent binding of a 62-kDa protein to the src
RT   homology 2 (SH2) domain of p56lck and its regulation by
RT   phosphorylation of Ser-59 in the lck unique N-terminal region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).
RN   [17]
RP   INTERACTION WITH HIV-1 NEF.
RX   MEDLINE=96386556; PubMed=8794306;
RA   Greenway A.L., Azad A., Mills J., McPhee D.A.;
RT   "Human immunodeficiency virus type 1 Nef binds directly to LCK and
RT   mitogen-activated protein kinase, inhibiting kinase activity.";
RL   J. Virol. 70:6701-6708(1996).
RN   [18]
RP   REVIEW.
RX   PubMed=10848956;
RA   Isakov N., Biesinger B.;
RT   "Lck protein tyrosine kinase is a key regulator of T-cell activation
RT   and a target for signal intervention by Herpesvirus saimiri and other
RT   viral gene products.";
RL   Eur. J. Biochem. 267:3413-3421(2000).
RN   [19]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [20]
RP   MASS SPECTROMETRY.
RC   TISSUE=Mammary cancer;
RX   MEDLINE=21829512; PubMed=11840567;
RX   DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
RA   Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA   Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA   Zvelebil M.J.;
RT   "Cluster analysis of an extensive human breast cancer cell line
RT   protein expression map database.";
RL   Proteomics 2:212-223(2002).
RN   [21]
RP   INTERACTION WITH LIME1.
RX   PubMed=14610046; DOI=10.1084/jem.20031484;
RA   Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
RA   Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
RA   Horejsi V.;
RT   "LIME: a new membrane raft-associated adaptor protein involved in CD4
RT   and CD8 coreceptor signaling.";
RL   J. Exp. Med. 198:1453-1462(2003).
RN   [22]
RP   INTERACTION WITH LIME1.

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  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
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Db        485 TFDYLRSVL 493


RESULT 6
LCK_MOUSE
ID   LCK_MOUSE      STANDARD;      PRT;   508 AA.
AC   P06240; Q61794; Q61795; Q62320; Q91X65;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   25-OCT-2005, sequence version 3.
DT   07-MAR-2006, entry version 74.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).
GN   Name=Lck; Synonyms=Lsk-t;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;
RA   Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;
RT   "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and
RT   overexpressed in the murine T cell lymphoma LSTRA.";
RL   Cell 43:393-404(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86146842; PubMed=3081813;
RA   Voronova A.F., Sefton B.M.;
RT   "Expression of a new tyrosine protein kinase is stimulated by
RT   retrovirus promoter insertion.";
RL   Nature 319:682-685(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
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RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.
RX MEDLINE=88142832; PubMed=3501824;
RA Voronova A.F., Adler H.T., Sefton B.M.;
RT "Two lck transcripts containing different 5' untranslated regions are
RT present in T cells.";
RL Mol. Cell. Biol. 7:4407-4413(1987).
RN [7]
RP MUTAGENESIS OF TYR-504.
RX MEDLINE=88248001; PubMed=3380790;
RA Amrein K.E., Sefton B.M.;
RT "Avian reovirus mRNAs are nonfunctional in infected mouse cells:
RT translational basis for virus host-range restriction.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).
RN [8]
RP INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19
RP AND CYS-22.
RX MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;
RA Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,
RA Littman D.R.;
RT "Interaction of the unique N-terminal region of tyrosine kinase p56lck
RT with cytoplasmic domains of CD4 and CD8 is mediated by cysteine
RT motifs.";
RL Cell 60:755-765(1990).
RN [9]
RP MUTAGENESIS.
RX MEDLINE=93059694; PubMed=1279202;
RA Hurley T.R., Amrein K.E., Sefton B.M.;
RT "Creation and characterization of temperature-sensitive mutants of the
RT lck tyrosine protein kinase.";
RL J. Virol. 66:7406-7413(1992).
RN [10]
RP MUTAGENESIS OF LYS-272.
RX MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;
RA Abraham N., Miceli M.C., Parnes J.C., Veillette A.;
RT "Enhancement of T-cell responsiveness by the lymphocyte-specific
RT tyrosine protein kinase p56lck.";
RL Nature 350:62-66(1991).
RN [11]
RP MUTAGENESIS OF TYR-504.
RX MEDLINE=91219495; PubMed=1708890;
RA Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;
RT "Thymic tumorigenesis induced by overexpression of p56lck.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
RN [12]
RP PHOSPHORYLATION BY CSK.
RX PubMed=8371758; DOI=10.1038/365156a0;
RA Chow L.M., Fournel M., Davidson D., Veillette A.;
RT "Negative regulation of T-cell receptor signalling by tyrosine protein
RT kinase p50csk.";
RL Nature 365:156-160(1993).
RN [13]
RP MUTAGENESIS.
RX MEDLINE=93133805; PubMed=8421674;
RA Carrera A.C., Alexandrov K., Roberts T.M.;
RT "The conserved lysine of the catalytic domain of protein kinases is
RT actively involved in the phosphotransfer reaction and not required for
RT anchoring ATP.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
RN [14]
RP PALMITOYLATION.
RX MEDLINE=94019312; PubMed=8413237;
RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
RT "Palmitylation of an amino-terminal cysteine motif of protein tyrosine
RT kinases p56lck and p59fyn mediates interaction with glycosyl-
RT phosphatidylinositol-anchored proteins.";
RL Mol. Cell. Biol. 13:6385-6392(1993).
RN [15]
RP PALMITOYLATION.
RX MEDLINE=95071286; PubMed=7980442;
RA Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;
RT "Palmitoylation of multiple Src-family kinases at a homologous N-
RT terminal motif.";
RL Biochem. J. 303:749-753(1994).
RN [16]
RP INTERACTION WITH CBLB.
RX PubMed=10646608; DOI=10.1038/35003228;

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RA   Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,
RA   Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,
RA   Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,
RA   Penninger J.M.;
RT   "Negative regulation of lymphocyte activation and autoimmunity by the
RT   molecular adaptor Cbl-b.";
RL   Nature 403:211-216(2000).
RN   [17]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [18]
RP   PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.
RX   PubMed=15592455; DOI=10.1038/nbt1046;
RA   Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA   Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT   "Immunoaffinity profiling of tyrosine phosphorylation in cancer

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RESULT 7
LCK_SAISC
ID   LCK_SAISC      STANDARD;      PRT;   508 AA.
AC   Q95KR7;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 2.
DT   07-MAR-2006, entry version 26.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], ENZYME REGULATION, AND INTERACTION WITH
RP   SAIMIRINE HERPESVIRUS 2 TIP.
RC   TISSUE=T-cell;
RX   MEDLINE=21424508; PubMed=11533187;
RX   DOI=10.1128/JVI.75.19.9252-9261.2001;
RA   Greve T., Tamgueney G., Fleischer B., Fickenscher H., Broeker B.M.;
RT   "Downregulation of p56Lck tyrosine kinase activity in T cells of
RT   squirrel monkeys (Saimiri sciureus) correlates with the non-
RT   transforming and apathogenic properties of herpesvirus saimiri in its
RT   natural host.";
RL   J. Virol. 75:9252-9261(2001).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- ENZYME REGULATION: Regulated by phosphatases.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity). Interacts with saimirine herpesvirus 2 TIP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed specificaly in lymphoid cells.
CC   -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout
CC       T-cell ontogeny.
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This
CC       phosphorylation downregulates catalytic activity. Phosphorylated
CC       on Tyr-393 either by itself or another kinase, leading to
CC       increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   -!- CAUTION: LCK seems to be active in all vertebrates, except in
CC       squirrel monkey T-cells, in which it is inactivated. The reason
CC       seems to be that squirrel monkey are the natural host for
CC       Saimiriine herpesvirus 2, which is able to efficiently transform
CC       T-cells through a mecanism involving viral Tip/ host LCK
CC       interaction. Its inactivation may a mecanism that specificaly
CC       counteracts the transformation effects of viral Tip.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277921; CAC38871.1; -; mRNA.
DR   HSSP; P06239; 1LKK.
DR   SMR; Q95KR7; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
```

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KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088127.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58122 MW;  5088C64061853819 CRC64;

  Query Match             100.0%;  Score 45;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        485 TFDYLRSVL 493


RESULT 8
Q7RTZ3_HUMAN
ID   Q7RTZ3_HUMAN   PRELIMINARY;   PRT;   509 AA.
AC   Q7RTZ3;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Protein tyrosine kinase.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22289034; PubMed=12401726;
RA   Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,
RA   Naquet P., Matsuda F., Imbert J., Vialettes B.;
RT   "No association between lck gene polymorphisms and protein level in
RT   type 1 diabetes.";
RL   Diabetes 51:3326-3330(2002).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BN000073; CAD55807.1; -; Genomic_DNA.
DR   HSSP; P06239; 1BHF.
DR   SMR; Q7RTZ3; 65-509.
DR   Ensembl; ENSG00000182866; Homo sapiens.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   509 AA;  58001 MW;  44BFF0D43FFB420D CRC64;

  Query Match             100.0%;  Score 45;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        486 TFDYLRSVL 494


RESULT 9
Q95M32_9PRIM
ID   Q95M32_9PRIM   PRELIMINARY;   PRT;   509 AA.
AC   Q95M32;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Lck protein.
GN   Name=lck;
OS   Hylobates sp. (gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Hylobatidae; Hylobates.
OX   NCBI_TaxID=9581;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
RA   Picard C., Greenway A., Holloway G., Olive D., Collette Y.;
RT   "Interaction with simian Hck tyrosine kinase reveals convergent
RT   evolution of the Nef protein from simian and human immunodeficiency
RT   viruses despite differential molecular surface usage.";
RL   Virology 295:320-327(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Picard C.;
RL   Thesis (2001), Department of Experimental Oncology laboratory, U.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
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CC   ----------------------------------------------------------------------
DR   EMBL; AJ320182; CAC44027.1; -; mRNA.
DR   HSSP; P06239; 1LCK.
DR   SMR; Q95M32; 65-509.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   509 AA;  57947 MW;  F1BFE5C237C8DB7E CRC64;

  Query Match           100.0%;  Score 45;  DB 2;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 3.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        486 TFDYLRSVL 494


RESULT 10
Q3ZCM0_BOVIN
ID   Q3ZCM0_BOVIN   PRELIMINARY;   PRT;   509 AA.
AC   Q3ZCM0;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein MGC126900.
GN   Name=MGC126900;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; BC102046; AAI02047.1; -; mRNA.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   509 AA;  58116 MW;  CE0E80DCD6D0F2F8 CRC64;

  Query Match           100.0%;  Score 45;  DB 2;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 3.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        486 TFDYLRSVL 494


RESULT 11
Q573B4_HUMAN
ID   Q573B4_HUMAN   PRELIMINARY;   PRT;   516 AA.
AC   Q573B4;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Proto-oncogene tyrosine-protein kinase LCK.
```

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GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   PubMed=16107303; DOI=10.1016/j.gene.2005.06.018;
RA   Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,
RA   Naquet P., Imbert J.;
RT   "A rare mRNA variant of the human lymphocyte-specific protein tyrosine
RT   kinaseLCK gene with intron B retention and exon 7 skipping encodes a
RT   putativeprotein with altered SH3-dependent molecular interactions.";
RL   Gene 359:18-25(2005).
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ865079; CAI23831.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   516 AA;  58333 MW;  EB9A52D4EBDF14D2 CRC64;

  Query Match             100.0%;  Score 45;  DB 2;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||||||
Db        493 TFDYLRSVL 501


RESULT 12
Q9U8V6_EPTBU
ID   Q9U8V6_EPTBU   PRELIMINARY;   PRT;   249 AA.
AC   Q9U8V6;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like A (Fragment).
OS   Eptatretus burgeri (Inshore hagfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
OC   Myxinidae; Eptatretinae; Eptatretus.
OX   NCBI_TaxID=7764;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025546; BAA84736.1; -; mRNA.
DR   HSSP; P06239; 1QPC.
DR   SMR; Q9U8V6; 1-249.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   249 AA;  28636 MW;  D7F37EE197EA580C CRC64;

  Query Match             93.3%;  Score 42;  DB 2;  Length 249;
  Best Local Similarity   88.9%;  Pred. No. 6.3;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        226 TFDYLKSVL 234


RESULT 13
Q2UQK7_ASPOR
ID   Q2UQK7_ASPOR   PRELIMINARY;   PRT;   318 AA.
AC   Q2UQK7;
DT   24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT   24-JAN-2006, sequence version 1.
DT   07-MAR-2006, entry version 3.
DE   Predicted protein.
GN   ORFNames=AO090005001207;
OS   Aspergillus oryzae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5062;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=RIB 40;
RX   PubMed=16372010; DOI=10.1038/nature04300;
RA   Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
RA   Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
RA   Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA   Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
RA   Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,
RA   Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,
RA   Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA   Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA   Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA   Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
RA   Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
RA   Kuhara S., Ogasawara N., Kikuchi H.;
RT   "Genome sequencing and analysis of Aspergillus oryzae.";
RL   Nature 438:1157-1161(2005).
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
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DR   EMBL; AP007151; BAE56158.1; -; Genomic_DNA.
SQ   SEQUENCE   318 AA;  36042 MW;  E93277F08DD08AA1 CRC64;

  Query Match             91.1%;  Score 41;  DB 2;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSV 8
              ||||||||
Db        150 TFDYLRSV 157


RESULT 14
Q4RNX3_TETNG
ID   Q4RNX3_TETNG   PRELIMINARY;   PRT;   466 AA.
AC   Q4RNX3;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Chromosome 10 SCAF15009, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00031368001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01015009; CAG09909.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase.
FT   NON_TER     466    466
SQ   SEQUENCE   466 AA;  53437 MW;  E35D93F87395B799 CRC64;

  Query Match             91.1%;  Score 41;  DB 2;  Length 466;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              ||:||||||
Db        446 TFEYLRSVL 454


RESULT 15
O13064_XENLA
ID   O13064_XENLA   PRELIMINARY;   PRT;   488 AA.
AC   O13064;
DT   01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT   01-JUL-1997, sequence version 1.
DT   07-FEB-2006, entry version 29.
DE   Lyn protein tyrosine kinase.
GN   Name=Lyn;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fukami Y., Funabiki K., Sato K.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB003358; BAA20078.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; O13064; 43-488.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
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DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   488 AA;  55795 MW;  B7E70668B6EA92B2 CRC64;

  Query Match             91.1%;  Score 41;  DB 2;  Length 488;
  Best Local Similarity   88.9%;  Pred. No. 20;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        465 TFDYLQSVL 473


RESULT 16
Q3U6Q5_MOUSE
ID   Q3U6Q5_MOUSE   PRELIMINARY;   PRT;   491 AA.
AC   Q3U6Q5;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830119M13 product:Yamaguchi sarcoma viral (v-yes-1) oncogene
DE   homolog, full insert sequence.
GN   Name=Lyn;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AK153038; BAE31669.1; -; mRNA.
DR   MGI; MGI:96892; Lyn.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.

SQ   SEQUENCE   491 AA;  56285 MW;  2C82015D510B1F59 CRC64;

  Query Match             91.1%;  Score 41;  DB 2;  Length 491;
  Best Local Similarity   88.9%;  Pred. No. 20;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
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Db        468 TFDYLQSVL 476


RESULT 17
Q8CEI0_MOUSE
ID   Q8CEI0_MOUSE   PRELIMINARY;   PRT;   491 AA.
AC   Q8CEI0;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   10 day old male pancreas cDNA, RIKEN full-length enriched library,
DE   clone:1810073A02 product:Yamaguchi sarcoma viral (v-yes-1) oncogene
DE   homolog, full insert sequence.
GN   Name=Lyn;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
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RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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CC ---
DR EMBL; AK028112; BAC25753.1; -; mRNA.
DR HSSP; P08631; 1AD5.
DR SMR; Q8CEI0; 46-491.
DR Ensembl; ENSMUSG00000042228; Mus musculus.
DR MGI; MGI:96892; Lyn.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
DR GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3_1; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyrKc; 1.

Query Match 91.1%; Score 41; DB 2; Length 491;
Best Local Similarity 88.9%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db        468 TFDYLQSVL 476


RESULT 18
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ID   Q5ZMB9_CHICK   PRELIMINARY;   PRT;   492 AA.
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DT   23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT   23-NOV-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Hypothetical protein.
GN   ORFNames=RCJMB04_2j8;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CB; TISSUE=Bursa;
RA   Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA   Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA   Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT   "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT   genefunction analysis.";
RL   Genome Biol. 6:R6-R6(2005).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ719465; CAG31124.1; -; mRNA.
DR   SMR; Q5ZMB9; 46-492.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   492 AA;  56202 MW;  69D2F0534E33CC1E CRC64;

  Query Match             91.1%;  Score 41;  DB 2;  Length 492;
  Best Local Similarity   88.9%;  Pred. No. 20;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
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Db        469 TFDYLQSVL 477


RESULT 19
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ID   LYN_HUMAN      STANDARD;      PRT;   511 AA.
AC   P07948;
DT   01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1994, sequence version 2.
DT   07-MAR-2006, entry version 74.
DE   Tyrosine-protein kinase Lyn (EC 2.7.1.112).
GN   Name=LYN;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87172710; PubMed=3561390;
RA   Yamanashi Y., Fukushige S., Semba K., Sukegawa J., Miyajima N.,
RA   Matsubara K., Yamamoto T., Toyoshima K.;
RT   "The yes-related cellular gene lyn encodes a possible tyrosine kinase
RT   similar to p56lck.";
RL   Mol. Cell. Biol. 7:237-243(1987).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=94171041; PubMed=8125304; DOI=10.1016/0378-1119(94)90811-7;
RA   Rider L.G., Raben N., Miller L., Jelsema C.;
RT   "The cDNAs encoding two forms of the LYN protein tyrosine kinase are
RT   expressed in rat mast cells and human myeloid cells.";
RL   Gene 138:219-222(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LYN A).
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 368-423.
RX   MEDLINE=91062389; PubMed=2247464;
RA   Partanen J., Maekelae T.P., Alitalo R., Lehvaeslaiho H., Alitalo K.;
RT   "Putative tyrosine kinases expressed in K-562 human leukemia cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917(1990).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 368-423.
RX   MEDLINE=92378604; PubMed=1510669;
RA   Bielke W., Ziemieki A., Kappos L., Miescher G.C.;
RT   "Expression of the B cell-associated tyrosine kinase gene Lyn in
RT   primary neuroblastoma tumours and its modulation during the
RT   differentiation of neuroblastoma cell lines.";
RL   Biochem. Biophys. Res. Commun. 186:1403-1409(1992).
RN   [6]
RP   INTERACTION WITH EPSTEIN-BARR VIRUS LMP2A.
RX   PubMed=7895172;
RA   Miller C.L., Burkhardt A.L., Lee J.H., Stealey B., Longnecker R.,
RA   Bolen J.B., Kieff E.;
RT   "Integral membrane protein 2 of Epstein-Barr virus regulates
RT   reactivation from latency through dominant negative effects on
RT   protein-tyrosine kinases.";
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RL   Immunity 2:155-166(1995).
RN   [7]
RP   PHOSPHORYLATION SITE TYR-507, AND MASS SPECTROMETRY.
RX   PubMed=15592455; DOI=10.1038/nbt1046;
RA   Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA   Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT   "Immunoaffinity profiling of tyrosine phosphorylation in cancer
RT   cells.";
RL   Nat. Biotechnol. 23:94-101(2005).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.
CC       Interacts with Epstein-Barr virus LMP2A.
CC   -!- INTERACTION:
CC       O92969:- (xeno); NbExp=2; IntAct=EBI-79452, EBI-710506;
CC       P26660:- (xeno); NbExp=1; IntAct=EBI-79452, EBI-706322;
CC       P27958:- (xeno); NbExp=5; IntAct=EBI-79452, EBI-706378;
CC       Q9WMX2:- (xeno); NbExp=2; IntAct=EBI-79452, EBI-710918;
CC       P20273:CD22; NbExp=1; IntAct=EBI-79452, EBI-78277;
CC       Q6NVF1:Centd3 (xeno); NbExp=2; IntAct=EBI-79452, EBI-621463;
CC       P67870:CSNK2B; NbExp=1; IntAct=EBI-79452, EBI-348169;
CC       Q9UIF2:gpVI; NbExp=2; IntAct=EBI-79452, EBI-515278;
CC       Q07666:KHDRBS1; NbExp=1; IntAct=EBI-79452, EBI-1364;
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LYN A;
CC         IsoId=P07948-1; Sequence=Displayed;
CC       Name=LYN B;
CC         IsoId=P07948-2; Sequence=VSP_005002;
CC   -!- TISSUE SPECIFICITY: Expressed in primary neuroblastoma tumors.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; M16038; AAA59540.1; -; mRNA.
DR   EMBL; M79321; AAB50019.1; -; mRNA.
DR   EMBL; BC075001; AAH75001.1; -; mRNA.
DR   EMBL; BC075002; AAH75002.1; -; mRNA.
DR   PIR; A26719; TVHULY.
DR   PDB; 1W1F; NMR; A=60-122.
DR   PDB; 1WA7; NMR; A=60-122.
DR   SMR; P07948; 66-511.
DR   IntAct; P07948; -.
DR   Ensembl; ENSG00000147507; Homo sapiens.
DR   HGNC; HGNC:6735; LYN.
DR   MIM; 165120; gene.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . .; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   3D-structure; Alternative splicing; ATP-binding; Kinase; Lipoprotein;
KW   Myristate; Nucleotide-binding; Palmitate; Phosphorylation;
KW   Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    511       Tyrosine-protein kinase Lyn.
FT                                /FTId=PRO_0000088129.
FT   DOMAIN       62    122       SH3.
FT   DOMAIN      128    225       SH2.
FT   DOMAIN      246    500       Protein kinase.
FT   NP_BIND     252    260       ATP (By similarity).
FT   ACT_SITE    366    366       Proton acceptor (By similarity).
FT   BINDING     274    274       ATP (By similarity).
FT   MOD_RES     396    396       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     507    507       Phosphotyrosine.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   VARSPLIC     22     42       Missing (in isoform LYN B).
FT                                /FTId=VSP_005002.
FT   STRAND       65     71
FT   STRAND       73     73
FT   STRAND       77     79
FT   STRAND       83     83
FT   TURN         85     86
FT   STRAND       88     94
FT   STRAND       96    103
FT   TURN        104    106
FT   STRAND      109    113
FT   TURN        114    116
FT   STRAND      117    119
SQ   SEQUENCE   511 AA;  58443 MW;  8419CD461204E364 CRC64;

  Query Match             91.1%;  Score 41;  DB 1;  Length 511;
  Best Local Similarity   88.9%;  Pred. No. 21;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        488 TFDYLQSVL 496


RESULT 20
LYN_MOUSE
ID   LYN_MOUSE      STANDARD;      PRT;   511 AA.
AC   P25911; Q62127;
DT   01-MAY-1992, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1997, sequence version 3.
DT   07-MAR-2006, entry version 64.
DE   Tyrosine-protein kinase Lyn (EC 2.7.1.112).
GN   Name=Lyn;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=91260688; PubMed=1710766;
RA   Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A., Lock P.,
RA   Dunn A.R.;
RT   "Alternatively spliced murine lyn mRNAs encode distinct proteins.";
RL   Mol. Cell. Biol. 11:3399-3406(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=91203857; PubMed=2017160;
RA   Yi T., Bolen J.B., Ihle J.N.;
RT   "Hematopoietic cells express two forms of lyn kinase differing by 21
RT   amino acids in the amino terminus.";
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RL   Mol. Cell. Biol. 11:2391-2398(1991).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LYN A).
RC   STRAIN=Czech II; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 363-431.
RX   MEDLINE=90152381; PubMed=2482828; DOI=10.1016/0378-1119(89)90465-4;
RA   Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
RT   "The application of the polymerase chain reaction to cloning members
RT   of the protein tyrosine kinase family.";
RL   Gene 85:67-74(1989).
RN   [5]
RP   INTERACTION WITH LIME1.
RX   PubMed=16249387; DOI=10.1182/blood-2005-05-1859;
RA   Ahn E., Lee H., Yun Y.;
RT   "LIME acts as a transmembrane adapter mediating BCR-dependent B-cell
RT   activation.";
RL   Blood 107:1521-1527(2006).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LYN A;
CC         IsoId=P25911-1; Sequence=Displayed;
CC       Name=LYN B;
CC         IsoId=P25911-2; Sequence=VSP_005003;
CC   -!- TISSUE SPECIFICITY: Expressed predominantly in B-lymphoid and
CC       myeloid cells.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; M64608; AAA39470.1; -; mRNA.
DR   EMBL; M57696; AAA39471.1; -; mRNA.
DR   EMBL; M57697; AAA39472.1; -; mRNA.
DR   EMBL; BC031547; AAH31547.1; -; mRNA.
DR   EMBL; M33426; AAA40017.1; -; mRNA.
DR   PIR; A39719; A39719.
DR   HSSP; P08631; 1AD5.
DR   SMR; P25911; 66-511.
DR   IntAct; P25911; -.
DR   Ensembl; ENSMUSG00000042228; Mus musculus.
DR   MGI; MGI:96892; Lyn.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR   GO; GO:0046777; P:autophosphorylation; IDA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Alternative splicing; ATP-binding; Kinase; Lipoprotein; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    511       Tyrosine-protein kinase Lyn.
FT                                /FTId=PRO_0000088130.
FT   DOMAIN       62    122       SH3.
FT   DOMAIN      128    225       SH2.
FT   DOMAIN      246    500       Protein kinase.
FT   NP_BIND     252    260       ATP (By similarity).
FT   ACT_SITE    366    366       Proton acceptor (By similarity).
FT   BINDING     274    274       ATP (By similarity).
FT   MOD_RES     396    396       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     507    507       Phosphotyrosine (By similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   VARSPLIC     24     44       Missing (in isoform LYN B).
FT                                /FTId=VSP_005003.
FT   CONFLICT     76     76       I -> F (in Ref. 2).
FT   CONFLICT    160    160       L -> I (in Ref. 2).
FT   CONFLICT    278    278       P -> L (in Ref. 2).
FT   CONFLICT    390    390       V -> I (in Ref. 2).
FT   CONFLICT    414    414       I -> F (in Ref. 4).
FT   CONFLICT    424    424       D -> N (in Ref. 1).
FT   CONFLICT    431    431       L -> P (in Ref. 4).
SQ   SEQUENCE   511 AA;  58681 MW;  3935221CC90C50F0 CRC64;

  Query Match             91.1%;  Score 41;  DB 1;  Length 511;
  Best Local Similarity   88.9%;  Pred. No. 21;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        488 TFDYLQSVL 496


RESULT 21
LYN_RAT
ID   LYN_RAT        STANDARD;      PRT;   511 AA.
AC   Q07014; Q63320;
DT   01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1997, sequence version 2.
DT   07-MAR-2006, entry version 57.
DE   Tyrosine-protein kinase Lyn (EC 2.7.1.112).
GN   Name=Lyn;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Minoguchi K., Nishikata H., Siraganian R.P.;
RT   "Bacterially expressed rat p56lyn binds several proteins in rat
RT   basophilic leukemia cells including pp72, a tyrosine phosphorylated
RT   protein prominent in activated cells.";
RL   J. Immunol. 150:222-222(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=94171041; PubMed=8125304; DOI=10.1016/0378-1119(94)90811-7;
RA   Rider L.G., Raben N., Miller L., Jelsema C.;
RT   "The cDNAs encoding two forms of the LYN protein tyrosine kinase are
RT   expressed in rat mast cells and human myeloid cells.";
RL   Gene 138:219-222(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=97442484; PubMed=9295361; DOI=10.1074/jbc.272.38.24072;
RA   Vonakis B.M., Chen H., Haleem-Smith H., Metzger H.;
RT   "The unique domain as the site on Lyn kinase for its constitutive
RT   association with the high affinity receptor for IgE.";
RL   J. Biol. Chem. 272:24072-24080(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LYN A;
CC         IsoId=Q07014-1; Sequence=Displayed;
CC       Name=LYN B;
CC         IsoId=Q07014-2; Sequence=VSP_005004;
CC   -!- TISSUE SPECIFICITY: Expressed predominantly in B-lymphoid and
CC       myeloid cells.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; L14951; AAA41549.1; -; mRNA.
DR   EMBL; L14782; AAA20944.1; -; mRNA.
DR   EMBL; L14823; AAA20945.1; -; mRNA.
DR   EMBL; AF000300; AAB71344.1; -; mRNA.
DR   EMBL; AF000301; AAB71345.1; -; mRNA.
DR   EMBL; AF000302; AAB71346.1; -; mRNA.
DR   PIR; I56160; I56160.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q07014; 66-511.
DR   Ensembl; ENSRNOG00000008180; Rattus norvegicus.
DR   RGD; 621017; Lyn.
DR   GO; GO:0016301; F:kinase activity; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Alternative splicing; ATP-binding; Kinase; Lipoprotein; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    511       Tyrosine-protein kinase Lyn.
FT                                /FTId=PRO_0000088131.
FT   DOMAIN       62    122       SH3.
FT   DOMAIN      128    225       SH2.
FT   DOMAIN      246    500       Protein kinase.
FT   NP_BIND     252    260       ATP (By similarity).
FT   ACT_SITE    366    366       Proton acceptor (By similarity).
FT   BINDING     274    274       ATP (By similarity).
FT   MOD_RES     396    396       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     507    507       Phosphotyrosine (By similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   VARSPLIC     24     44       Missing (in isoform LYN B).
FT                                /FTId=VSP_005004.
FT   CONFLICT    230    230       P -> L (in Ref. 2).
FT   CONFLICT    307    307       V -> A (in Ref. 2).
FT   CONFLICT    418    418       C -> Y (in Ref. 2).
SQ   SEQUENCE   511 AA;  58529 MW;  24A2E5E229CD43ED CRC64;

  Query Match             91.1%;  Score 41;  DB 1;  Length 511;
  Best Local Similarity   88.9%;  Pred. No. 21;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        488 TFDYLQSVL 496


RESULT 22
Q3TCS3_MOUSE
ID   Q3TCS3_MOUSE   PRELIMINARY;   PRT;   512 AA.
AC   Q3TCS3;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched
DE   library, clone:F630107O15 product:Yamaguchi sarcoma viral (v-yes-1)
DE   oncogene homolog, full insert sequence (Bone marrow macrophage cDNA,
DE   RIKEN full-length enriched library, clone:I830054M12 product:Yamaguchi
DE   sarcoma viral (v-yes-1) oncogene homolog, full insert sequence).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
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RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AK170561; BAE41882.1; -; mRNA.
DR EMBL; AK152199; BAE31028.1; -; mRNA.
DR GO; GO:0005515; F:protein binding; IPI.

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DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.

  Query Match             91.1%;  Score 41;  DB 2;  Length 512;
  Best Local Similarity   88.9%;  Pred. No. 21;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        489 TFDYLQSVL 497


RESULT 23
Q6NUK7_HUMAN
ID   Q6NUK7_HUMAN   PRELIMINARY;   PRT;   582 AA.
AC   Q6NUK7;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   LYN protein (Fragment).
GN   Name=LYN;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May serve as part of a signaling pathway coupling the Fc
CC       receptor to the activation of the respiratory burst. May also
CC       contribute to neutrophil migration and may regulate the
CC       degranulation process of neutrophils (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC068551; AAH68551.1; -; mRNA.
DR   EMBL; BC059394; AAH59394.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q6NUK7; 24-86, 137-582.
DR   Ensembl; ENSG00000147507; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000108; Neu_cyt_fact_2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00499; P67PHOX.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1       1
SQ   SEQUENCE   582 AA;  65809 MW;  1CFF99768C28E9BB CRC64;

  Query Match             91.1%;  Score 41;  DB 2;  Length 582;
  Best Local Similarity   88.9%;  Pred. No. 24;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||:|||
Db        559 TFDYLQSVL 567


RESULT 24
Q66I04_BRARE
ID   Q66I04_BRARE   PRELIMINARY;   PRT;   510 AA.
AC   Q66I04;
DT   11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
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DE   Zgc:92124.
GN   ORFNames=zgc:92124;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC081601; AAH81601.1; -; mRNA.
DR   SMR; Q66I04; 65-510.
DR   Ensembl; ENSDARG00000031715; Danio rerio.
DR   ZFIN; ZDB-GENE-040912-7; zgc:92124.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   510 AA;  58258 MW;  5EE8F68226569BA2 CRC64;
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  Query Match           86.7%;  Score 39;  DB 2;  Length 510;
  Best Local Similarity   77.8%;  Pred. No. 54;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
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Db        487 TFDYIQSVL 495


RESULT 25
Q4X0L1_ASPFU
ID   Q4X0L1_ASPFU   PRELIMINARY;   PRT;   605 AA.
AC   Q4X0L1;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein.
GN   ORFNames=Afu2g13100;
OS   Aspergillus fumigatus (Sartorya fumigata).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5085;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Af293 / CBS 101355 / FGSC A1100;
RX   PubMed=16372009; DOI=10.1038/nature04332;
RA   Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
RA   Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
RA   Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
RA   Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
RA   Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA   Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
RA   Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,
RA   Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
RA   Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A.,
RA   Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
RA   Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,
RA   Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA   Rabbinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
RA   Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA   Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA   Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA   Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA   White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,
RA   Machida M., Hall N., Barrell B.G., Denning D.W.;
RT   "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT   Aspergillus fumigatus.";
RL   Nature 438:1151-1156(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAHF01000001; EAL93604.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   605 AA;  67156 MW;  086740E5B9FFC1AE CRC64;

  Query Match           84.4%;  Score 38;  DB 2;  Length 605;
  Best Local Similarity   87.5%;  Pred. No. 1e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSV 8
              |:||||||
Db        558 TYDYLRSV 565


RESULT 26
Q5AZN3_EMENI
ID   Q5AZN3_EMENI   PRELIMINARY;   PRT;   606 AA.
AC   Q5AZN3;
DT   26-APR-2005, integrated into UniProtKB/TrEMBL.
```

```
DT   26-APR-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein.
GN   ORFNames=AN6247.2;
OS   Aspergillus nidulans FGSC A4.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=227321;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=FGSC 4;
RX   PubMed=16372000; DOI=10.1038/nature04341;
RA   Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
RA   Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
RA   Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,
RA   Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C.,
RA   Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
RA   Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,
RA   Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
RA   Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
RA   Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,
RA   Sachs M.S., Osmani S.A., Birren B.W.;
RT   "Sequencing of Aspergillus nidulans and comparative analysis with A.
RT   fumigatus and A. oryzae.";
RL   Nature 438:1105-1115(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ---------------------------------------------------------------------
DR   EMBL; AACD01000107; EAA58631.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   606 AA;  67119 MW;  A95532E982BF7A8E CRC64;

  Query Match             84.4%;  Score 38;  DB 2;  Length 606;
  Best Local Similarity   87.5%;  Pred. No. 1e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSV 8
              |:||||||
Db        560 TYDYLRSV 567


RESULT 27
Q86TW9_HUMAN
ID   Q86TW9_HUMAN   PRELIMINARY;   PRT;    98 AA.
AC   Q86TW9;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Full-length cDNA clone CS0DI065YF14 of Placenta of Homo sapiens
DE   (human) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RA   Li W.B., Gruber C., Jessee J., Polayes D.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RA   Genoscope;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BX248053; CAD62355.1; -; mRNA.
DR   Ensembl; ENSG00000119688; Homo sapiens.
FT   NON_TER      98     98
SQ   SEQUENCE   98 AA;  10702 MW;  B5072D6E7DADBFB8 CRC64;

  Query Match             82.2%;  Score 37;  DB 2;  Length 98;
  Best Local Similarity   77.8%;  Pred. No. 25;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||  |:|
Db         13 TFDYLGSIL 21


RESULT 28
Q5FWT4_RAT
ID   Q5FWT4_RAT     PRELIMINARY;   PRT;   267 AA.
AC   Q5FWT4;
DT   01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2005, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   ATP-binding cassette, sub-family D (ALD), member 4 (Predicted).
GN   Name=Abcd4;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RG   NIH MGC Project;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC089214; AAH89214.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
KW   ATP-binding.
SQ   SEQUENCE   267 AA;  29257 MW;  FA84B1C7FBB5B3D5 CRC64;

  Query Match             82.2%;  Score 37;  DB 2;  Length 267;
  Best Local Similarity   77.8%;  Pred. No. 71;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TFDYLRSVL 9
              |||||  |:|
Db         50 TFDYLGSIL 58
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RESULT 29
Q8YMU7_ANASP
ID   Q8YMU7_ANASP   PRELIMINARY;   PRT;   379 AA.
AC   Q8YMU7;
DT   01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2002, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Mannosyl transferase.
GN   OrderedLocusNames=all4830;
OS   Anabaena sp. (strain PCC 7120).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX   NCBI_TaxID=103690;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=21595285; PubMed=11759840; DOI=10.1093/dnares/8.5.205;
RA   Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA   Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA   Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA   Yasuda M., Tabata S.;
RT   "Complete genomic sequence of the filamentous nitrogen-fixing
RT   cyanobacterium Anabaena sp. strain PCC 7120.";
RL   DNA Res. 8:205-213(2001).
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CC   ---------------------------------------------------------------------
DR   EMBL; BA000019; BAB76529.1; -; Genomic_DNA.
DR   PIR; AF2409; AF2409.
DR   BioCyc; NSP103690:ALL4830-MONOMER; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0009058; P:biosynthesis; IEA.
DR   InterPro; IPR001296; Glyco_trans_1.
DR   Pfam; PF00534; Glycos_transf_1; 1.
KW   Complete proteome; Transferase.
SQ   SEQUENCE   379 AA;  43514 MW;  12BD846E01CAA44D CRC64;

  Query Match             82.2%;  Score 37;  DB 2;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRS 7
              |||||||
Db        124 TFDYLRS 130


RESULT 30
Q3MBB4_ANAVT
ID   Q3MBB4_ANAVT   PRELIMINARY;   PRT;   381 AA.
AC   Q3MBB4;
DT   25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   25-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Glycosyl transferase, group 1.
GN   ORFNames=Ava_2100;
OS   Anabaena variabilis (strain ATCC 29413).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX   NCBI_TaxID=240292;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 29413;
RG   US DOE Joint Genome Institute;
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Saunders E.H., Schmutz J.,
RA   Larimer F., Land M., Kyrpides N., Mavrommatis K., Richardson P.;
RT   "Complete sequence of Anabaena variabilis ATCC 29413.";
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; CP000117; ABA21722.1; -; Genomic_DNA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0009058; P:biosynthesis; IEA.
DR   InterPro; IPR001296; Glyco_trans_1.
DR   Pfam; PF00534; Glycos_transf_1; 1.
KW   Transferase.
SQ   SEQUENCE   381 AA;  43616 MW;  881A8010B2BB24B6 CRC64;

  Query Match             82.2%;  Score 37;  DB 2;  Length 381;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFDYLRS 7
              |||||||
Db        126 TFDYLRS 132


Search completed: June 29, 2006, 09:29:35
Job time : 109.942 secs
```

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 117.59 Seconds
(without alignments)
78.664 Million cell updates/sec

Title: US-10-062-257A-2
Perfect score: 51
Sequence: 1 DYLRSVLEDF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	502	2	Q8QGJ9_FUGRU	Q8qgj9 fugu rubrip
2	51	100.0	508	1	LCK_AOTNA	Q5pxs1 aotus nancy
3	51	100.0	508	1	LCK_HUMAN	P06239 homo sapien
4	51	100.0	508	1	LCK_SAISC	Q95kr7 saimiri sci
5	51	100.0	509	2	Q7RTZ3_HUMAN	Q7rtz3 homo sapien
6	51	100.0	509	2	Q95M32_9PRIM	Q95m32 hylobates s
7	51	100.0	509	2	Q3ZCM0_BOVIN	Q3zcm0 bos taurus
8	51	100.0	516	2	Q573B4_HUMAN	Q573b4 homo sapien
9	48	94.1	249	2	Q9U8V6_EPTBU	Q9u8v6 eptatretus
10	48	94.1	368	2	Q3TLX4_MOUSE	Q3tlx4 mus musculu
11	48	94.1	379	2	Q4FZR6_RAT	Q4fzr6 rattus norv
12	48	94.1	508	1	LCK_MOUSE	P06240 mus musculu
13	47	92.2	466	2	Q4RNX3_TETNG	Q4rnx3 tetraodon n
14	44	86.3	488	2	O13064_XENLA	O13064 xenopus lae
15	44	86.3	491	2	Q3U6Q5_MOUSE	Q3u6q5 mus musculu
16	44	86.3	491	2	Q8CEI0_MOUSE	Q8cei0 mus musculu
17	44	86.3	492	2	Q5ZMB9_CHICK	Q5zmb9 gallus gall
18	44	86.3	511	1	LYN_HUMAN	P07948 homo sapien
19	44	86.3	511	1	LYN_MOUSE	P25911 mus musculu
20	44	86.3	511	1	LYN_RAT	Q07014 rattus norv
21	44	86.3	512	2	Q3TCS3_MOUSE	Q3tcs3 m nod-deriv
22	44	86.3	582	2	Q6NUK7_HUMAN	Q6nuk7 homo sapien
23	43	84.3	502	2	Q9DDK6_SALSA	Q9ddk6 salmo salar
24	43	84.3	503	2	Q6TPQ4_BRARE	Q6tpq4 brachydanio
25	42	82.4	496	2	O93411_XENLA	O93411 xenopus lae
26	42	82.4	507	1	LCK_CHICK	P42683 gallus gall
27	42	82.4	510	2	Q66I04_BRARE	Q66i04 brachydanio
28	40	78.4	196	2	Q5RHX5_BRARE	Q5rhx5 brachydanio
29	40	78.4	280	1	DCNL4_BRARE	Q5rhx6 brachydanio
30	40	78.4	281	2	Q4RKU7_TETNG	Q4rku7 tetraodon n
31	40	78.4	396	2	Q3A1V4_PELCD	Q3a1v4 pelobacter
32	40	78.4	509	1	STK_HYDAT	P17713 hydra atten
33	39	76.5	248	2	Q9VWB1_DROME	Q9vwb1 drosophila
34	39	76.5	498	1	BLK_MOUSE	P16277 mus musculu
35	39	76.5	498	2	Q5FW27_XENTR	Q5fw27 xenopus tro
36	39	76.5	499	2	Q3TAT8_MOUSE	Q3tat8 mus musculu
37	39	76.5	499	2	Q4KM97_RAT	Q4km97 rattus norv
38	39	76.5	499	2	Q8K2M8_MOUSE	Q8k2m8 mus musculu
39	39	76.5	504	1	BLK_HUMAN	P51451 homo sapien
40	39	76.5	505	2	Q96IN1_HUMAN	Q96in1 homo sapien
41	39	76.5	511	2	Q5UQF6_MIMIV	Q5uqf6 mimivirus.
42	39	76.5	514	2	Q4CEL0_CLOTM	Q4cel0 clostridium
43	39	76.5	2874	2	Q4QEZ2_LEIMA	Q4qez2 leishmania
44	38	74.5	132	2	Q8TZE4_PYRFU	Q8tze4 pyrococcus
45	38	74.5	184	2	Q9RLI6_PSEAE	Q9rli6 pseudomonas
46	38	74.5	260	2	Q6CEC5_YARLI	Q6cec5 yarrowia li
47	38	74.5	340	2	Q2SKX5_9GAMM	Q2skx5 hahella che
48	38	74.5	364	2	Q7MSC2_WOLSU	Q7msc2 wolinella s
49	38	74.5	377	2	Q6IND8_XENLA	Q6ind8 xenopus lae
50	38	74.5	403	2	Q331Q6_9ACTO	Q331q6 streptomyce
51	38	74.5	455	2	Q93SR8_PSEPU	Q93sr8 pseudomonas
52	38	74.5	455	2	Q9I0W4_PSEAE	Q9i0w4 pseudomonas
53	38	74.5	502	1	HCK_RAT	P50545 rattus norv
54	38	74.5	503	1	HCK_MACFA	Q95m30 macaca fasc
55	38	74.5	503	2	Q3UD17_MOUSE	Q3ud17 m bone marr
56	38	74.5	503	2	Q6AYV7_RAT	Q6ayv7 rattus norv
57	38	74.5	523	1	HCK_MOUSE	P08103 mus musculu
58	38	74.5	525	1	HCK_HUMAN	P08631 homo sapien
59	38	74.5	528	2	Q4WN83_ASPFU	Q4wn83 aspergillus
60	38	74.5	570	2	Q504R5_HUMAN	Q504r5 homo sapien
61	38	74.5	580	2	Q2VPE2_HUMAN	Q2vpe2 homo sapien
62	38	74.5	784	2	Q9XEI0_STERE	Q9xei0 stevia reba
63	38	74.5	789	1	KSB_CUCMA	Q39548 cucurbita m
64	38	74.5	858	2	Q98EU9_RHILO	Q98eu9 rhizobium l
65	38	74.5	891	2	Q8S5V3_ORYSA	Q8s5v3 oryza sativ
66	38	74.5	945	1	SYL1_SULTO	Q974n4 sulfolobus
67	38	74.5	1015	2	Q2UCT3_ASPOR	Q2uct3 aspergillus
68	38	74.5	1627	2	Q4I6Q6_GIBZE	Q4i6q6 gibberella
69	38	74.5	2343	2	Q75DB8_ASHGO	Q75db8 ashbya goss
70	37	72.5	63	2	Q58N37_9CAUD	Q58n37 cyanophage
71	37	72.5	100	2	Q5NZP9_AZOSE	Q5nzp9 azoarcus sp
72	37	72.5	262	2	Q3E7J1_ARATH	Q3e7j1 arabidopsis
73	37	72.5	292	1	DCNL4_MOUSE	Q8cca0 mus musculu
74	37	72.5	292	2	Q2YDW5_MOUSE	Q2ydw5 mus musculu
75	37	72.5	303	2	Q57U12_9TRYP	Q57u12 trypanosoma
76	37	72.5	303	2	Q57U14_9TRYP	Q57u14 trypanosoma
77	37	72.5	306	2	Q8C5X2_MOUSE	Q8c5x2 mus musculu
78	37	72.5	330	2	Q57U10_9TRYP	Q57u10 trypanosoma
79	37	72.5	356	2	Q57U16_9TRYP	Q57u16 trypanosoma
80	37	72.5	358	2	Q8S8M6_ARATH	Q8s8m6 arabidopsis
81	37	72.5	361	2	Q8RY40_ARATH	Q8ry40 arabidopsis
82	37	72.5	367	2	Q4RT53_TETNG	Q4rt53 tetraodon n
83	37	72.5	382	2	Q57U18_9TRYP	Q57u18 trypanosoma
84	37	72.5	384	2	Q4RY25_TETNG	Q4ry25 tetraodon n
85	37	72.5	453	2	P74763_SULSH	P74763 sulfolobus
86	37	72.5	696	2	Q3INU8_NATPD	Q3inu8 natronomona
87	37	72.5	710	2	Q8XTF2_RALSO	Q8xtf2 ralstonia s
88	37	72.5	959	2	Q871I6_NEUCR	Q871i6 neurospora
89	37	72.5	1444	2	Q4Y0H3_PLACH	Q4y0h3 plasmodium
90	37	72.5	2268	2	Q8I4N5_PLAF7	Q8i4n5 plasmodium
91	36	70.6	106	2	Q9ABV5_CAUCR	Q9abv5 caulobacter
92	36	70.6	127	2	Q3AP22_CHLCH	Q3ap22 chlorobium
93	36	70.6	158	2	Q54Z48_DICDI	Q54z48 dictyosteli
94	36	70.6	163	1	Y1021_METJA	Q58427 methanococc
95	36	70.6	187	2	Q8T3P7_DROME	Q8t3p7 drosophila
96	36	70.6	187	2	Q9VI77_DROME	Q9vi77 drosophila
97	36	70.6	202	2	Q96XM3_SULTO	Q96xm3 sulfolobus
98	36	70.6	238	2	Q6ZEP6_SYNY3	Q6zep6 synechocyst
99	36	70.6	249	2	Q9PVV0_LAMRE	Q9pvv0 lampetra re
100	36	70.6	255	2	Q5HUF1_CAMJR	Q5huf1 campylobact

ALIGNMENTS

```
RESULT 1
Q8QGJ9_FUGRU
ID   Q8QGJ9_FUGRU   PRELIMINARY;   PRT;   502 AA.
AC   Q8QGJ9;
DT   01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2002, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   Lymphocyte-specific c-src family protein tyrosine kinase.
GN   Name=lck;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21874085; PubMed=11867707; DOI=10.1073/pnas.032680599;
RA   Brenner S., Venkatesh B., Yap W.-H., Chou C.-F., Tay A.W.N.,
RA   Ponniah S., Wang Y., Tan Y.H.;
RT   "Conserved regulation of the lymphocyte-specific expression of lck in
RT   the Fugu and mammals.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:2936-2941(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF411956; AAL89664.1; -; Genomic_DNA.
DR   HSSP; P06239; 1QPC.
DR   Ensembl; SINFRUG00000129447; Fugu rubripes.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   502 AA;  57477 MW;  A8C9EC2E774F79CD CRC64;

  Query Match             100.0%;  Score 51;  DB 2;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        483 DYLRSVLEDF 492


RESULT 2
LCK_AOTNA
ID   LCK_AOTNA      STANDARD;      PRT;   508 AA.
AC   Q5PXS1;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 3.
DT   07-MAR-2006, entry version 13.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Perez-Quintero L.A., Vernot J.P.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY821852; AAV70114.2; -; mRNA.
DR   SMR; Q5PXS1; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
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DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088123.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58041 MW;  8B61951BC192A3A4 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        487 DYLRSVLEDF 496


RESULT 3
LCK_HUMAN
ID   LCK_HUMAN      STANDARD;      PRT;   508 AA.
AC   P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 5.
DT   07-MAR-2006, entry version 87.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK).
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-
DE   specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87133831; PubMed=3493153;
RA   Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
RA   Mak T.W.;
RT   "A human T cell-specific cDNA clone (YT16) encodes a protein with
RT   extensive homology to a family of protein-tyrosine kinases.";
RL   Eur. J. Immunol. 16:1643-1646(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89123626; PubMed=3265417;
RA   Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
RA   Wilson C.B.;
RT   "Structure and expression of lck transcripts in human lymphoid
RT   cells.";
RL   J. Cell. Biochem. 38:117-126(1988).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
RA   Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
RA   Benarous R.;
RT   "Structure of the human lck gene: differences in genomic organisation
RT   within src-related genes affect only N-terminal exons.";
RL   Gene 84:105-113(1989).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;
RP   VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.
RC   TISSUE=Leukemia;
RX   MEDLINE=94187714; PubMed=8139546;
RA   Wright D.D., Sefton B.M., Kamps M.P.;
RT   "Oncogenic activation of the Lck protein accompanies translocation of
RT   the LCK gene in the human HSB2 T-cell leukemia.";
RL   Mol. Cell. Biol. 14:2429-2437(1994).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.
RC   TISSUE=Leukemic T-cell;
RX   MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
RA   Vogel L.B., Arthur R., Fujita D.J.;
RT   "An aberrant lck mRNA in two human T-cell lines.";
RL   Biochim. Biophys. Acta 1264:168-172(1995).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   Human chromosome 1 international sequencing consortium;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89096891; PubMed=2850479;
RA   Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT   "Structure of the murine lck gene and its rearrangement in a murine
RT   lymphoma cell line.";
RL   Mol. Cell. Biol. 8:3058-3064(1988).
RN   [9]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89313764; PubMed=2787474;
RA   Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA   Miyamoto N.G., Mak T.W.;
RT   "Structure of the two promoters of the human lck gene: differential
RT   accumulation of two classes of lck transcripts in T cells.";
RL   Mol. Cell. Biol. 9:2173-2180(1989).
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RN   [10]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.
RC   TISSUE=Peripheral blood lymphocyte;
RX   MEDLINE=20462621; PubMed=11009097;
RX   DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
RA   Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S.,
RA   Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA   Baldari C.T.;
RT   "Defective recruitment and activation of ZAP-70 in common variable
RT   immunodeficiency patients with T cell defects.";
RL   Eur. J. Immunol. 30:2632-2638(2000).
RN   [11]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 367-508.
RX   MEDLINE=88217332; PubMed=2835736;
RA   Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RT   "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT   and other non-lymphoid human tumor cell lines.";
RL   Oncogene Res. 1:357-374(1987).
RN   [12]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 374-508.
RX   MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
RA   Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA   Linna T.J.;
RT   "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT   p56LSTRA.";
RL   Biochim. Biophys. Acta 888:286-295(1986).
RN   [13]
RP   PHOSPHORYLATION SITE TYR-504.
RX   MEDLINE=92347326; PubMed=1639064;
RA   Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA   Amrein K.E., Autero M., Burn P., Alitalo K.;
RT   "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT   down regulates its catalytic activity.";
RL   EMBO J. 11:2919-2924(1992).
RN   [14]
RP   INTERACTION WITH PI3K.
RX   MEDLINE=94067101; PubMed=7504174;
RA   Vogel L.B., Fujita D.J.;
RT   "The SH3 domain of p56lck is involved in binding to
RT   phosphatidylinositol 3'-kinase from T lymphocytes.";
RL   Mol. Cell. Biol. 13:7408-7417(1993).
RN   [15]
RP   INTERACTION WITH KHDRBS1.
RX   MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;
RA   Vogel L.B., Fujita D.J.;
RT   "p70 phosphorylation and binding to p56lck is an early event in
RT   interleukin-2-induced onset of cell cycle progression in T-
RT   lymphocytes.";
RL   J. Biol. Chem. 270:2506-2511(1995).
RN   [16]
RP   INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.
RX   PubMed=8618896;
RA   Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;
RT   "Phosphotyrosine-independent binding of a 62-kDa protein to the src
RT   homology 2 (SH2) domain of p56lck and its regulation by
RT   phosphorylation of Ser-59 in the lck unique N-terminal region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).
RN   [17]
RP   INTERACTION WITH HIV-1 NEF.
RX   MEDLINE=96386556; PubMed=8794306;
RA   Greenway A.L., Azad A., Mills J., McPhee D.A.;
RT   "Human immunodeficiency virus type 1 Nef binds directly to LCK and
RT   mitogen-activated protein kinase, inhibiting kinase activity.";
RL   J. Virol. 70:6701-6708(1996).
RN   [18]
RP   REVIEW.
RX   PubMed=10848956;
RA   Isakov N., Biesinger B.;
RT   "Lck protein tyrosine kinase is a key regulator of T-cell activation
RT   and a target for signal intervention by Herpesvirus saimiri and other
RT   viral gene products.";
RL   Eur. J. Biochem. 267:3413-3421(2000).
RN   [19]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [20]
RP   MASS SPECTROMETRY.
RC   TISSUE=Mammary cancer;
RX   MEDLINE=21829512; PubMed=11840567;
RX   DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
RA   Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA   Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA   Zvelebil M.J.;
RT   "Cluster analysis of an extensive human breast cancer cell line
RT   protein expression map database.";
RL   Proteomics 2:212-223(2002).
RN   [21]
RP   INTERACTION WITH LIME1.
RX   PubMed=14610046; DOI=10.1084/jem.20031484;
RA   Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
RA   Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
RA   Horejsi V.;
RT   "LIME: a new membrane raft-associated adaptor protein involved in CD4
RT   and CD8 coreceptor signaling.";
RL   J. Exp. Med. 198:1453-1462(2003).
RN   [22]
RP   INTERACTION WITH LIME1.

  Query Match             100.0%;  Score 51;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        487 DYLRSVLEDF 496


RESULT 4
LCK_SAISC
ID   LCK_SAISC      STANDARD;      PRT;   508 AA.
AC   Q95KR7;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 2.
DT   07-MAR-2006, entry version 26.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], ENZYME REGULATION, AND INTERACTION WITH
RP   SAIMIRINE HERPESVIRUS 2 TIP.
RC   TISSUE=T-cell;
RX   MEDLINE=21424508; PubMed=11533187;
RX   DOI=10.1128/JVI.75.19.9252-9261.2001;
RA   Greve T., Tamgueney G., Fleischer B., Fickenscher H., Broeker B.M.;
RT   "Downregulation of p56Lck tyrosine kinase activity in T cells of
RT   squirrel monkeys (Saimiri sciureus) correlates with the non-
RT   transforming and apathogenic properties of herpesvirus saimiri in its
RT   natural host.";
RL   J. Virol. 75:9252-9261(2001).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
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CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- ENZYME REGULATION: Regulated by phosphatases.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity). Interacts with saimirine herpesvirus 2 TIP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed specificaly in lymphoid cells.
CC   -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout
CC       T-cell ontogeny.
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This
CC       phosphorylation downregulates catalytic activity. Phosphorylated
CC       on Tyr-393 either by itself or another kinase, leading to
CC       increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   -!- CAUTION: LCK seems to be active in all vertebrates, except in
CC       squirrel monkey T-cells, in which it is inactivated. The reason
CC       seems to be that squirrel monkey are the natural host for
CC       Saimiriine herpesvirus 2, which is able to efficiently transform
CC       T-cells through a mecanism involving viral Tip/ host LCK
CC       interaction. Its inactivation may a mecanism that specificaly
CC       counteracts the transformation effects of viral Tip.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277921; CAC38871.1; -; mRNA.
DR   HSSP; P06239; 1LKK.
DR   SMR; Q95KR7; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088127.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58122 MW;  5088C64061853819 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        487 DYLRSVLEDF 496


RESULT 5
Q7RTZ3_HUMAN
ID   Q7RTZ3_HUMAN   PRELIMINARY;   PRT;   509 AA.
AC   Q7RTZ3;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Protein tyrosine kinase.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22289034; PubMed=12401726;
RA   Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,
RA   Naquet P., Matsuda F., Imbert J., Vialettes B.;
RT   "No association between lck gene polymorphisms and protein level in
RT   type 1 diabetes.";
RL   Diabetes 51:3326-3330(2002).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BN000073; CAD55807.1; -; Genomic_DNA.
DR   HSSP; P06239; 1BHF.
DR   SMR; Q7RTZ3; 65-509.
DR   Ensembl; ENSG00000182866; Homo sapiens.
DR   GO; GO:0045121; C:lipid raft; ISS.
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DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   509 AA;  58001 MW;  44BFF0D43FFB420D CRC64;

  Query Match            100.0%;  Score 51;  DB 2;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        488 DYLRSVLEDF 497


RESULT 6
Q95M32_9PRIM
ID   Q95M32_9PRIM   PRELIMINARY;   PRT;   509 AA.
AC   Q95M32;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Lck protein.
GN   Name=lck;
OS   Hylobates sp. (gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Hylobatidae; Hylobates.
OX   NCBI_TaxID=9581;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
RA   Picard C., Greenway A., Holloway G., Olive D., Collette Y.;
RT   "Interaction with simian Hck tyrosine kinase reveals convergent
RT   evolution of the Nef protein from simian and human immunodeficiency
RT   viruses despite differential molecular surface usage.";
RL   Virology 295:320-327(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Picard C.;
RL   Thesis (2001), Department of Experimental Oncology laboratory, U.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ320182; CAC44027.1; -; mRNA.
DR   HSSP; P06239; 1LCK.
DR   SMR; Q95M32; 65-509.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   509 AA;  57947 MW;  F1BFE5C237C8DB7E CRC64;

  Query Match            100.0%;  Score 51;  DB 2;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        488 DYLRSVLEDF 497


RESULT 7
Q3ZCM0_BOVIN
ID   Q3ZCM0_BOVIN   PRELIMINARY;   PRT;   509 AA.
AC   Q3ZCM0;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein MGC126900.
GN   Name=MGC126900;
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OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC102046; AAI02047.1; -; mRNA.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   509 AA;  58116 MW;  CE0E80DCD6D0F2F8 CRC64;

  Query Match            100.0%;  Score 51;  DB 2;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        488 DYLRSVLEDF 497
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RESULT 8
Q573B4_HUMAN
ID   Q573B4_HUMAN   PRELIMINARY;   PRT;   516 AA.
AC   Q573B4;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Proto-oncogene tyrosine-protein kinase LCK.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   PubMed=16107303; DOI=10.1016/j.gene.2005.06.018;
RA   Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,
RA   Naquet P., Imbert J.;
RT   "A rare mRNA variant of the human lymphocyte-specific protein tyrosine
RT   kinaseLCK gene with intron B retention and exon 7 skipping encodes a
RT   putativeprotein with altered SH3-dependent molecular interactions.";
RL   Gene 359:18-25(2005).
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ865079; CAI23831.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   516 AA;  58333 MW;  EB9A52D4EBDF14D2 CRC64;

  Query Match            100.0%;  Score 51;  DB 2;  Length 516;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||||||||||
Db        495 DYLRSVLEDF 504


RESULT 9
Q9U8V6_EPTBU
ID   Q9U8V6_EPTBU   PRELIMINARY;   PRT;   249 AA.
AC   Q9U8V6;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like A (Fragment).
OS   Eptatretus burgeri (Inshore hagfish).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
OC   Myxinidae; Eptatretinae; Eptatretus.
OX   NCBI_TaxID=7764;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025546; BAA84736.1; -; mRNA.
DR   HSSP; P06239; 1QPC.
DR   SMR; Q9U8V6; 1-249.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   249 AA;  28636 MW;  D7F37EE197EA580C CRC64;

  Query Match             94.1%;  Score 48;  DB 2;  Length 249;
  Best Local Similarity   90.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              |||:||||||
Db        228 DYLKSVLEDF 237


RESULT 10
Q3TLX4_MOUSE
ID   Q3TLX4_MOUSE   PRELIMINARY;   PRT;   368 AA.
AC   Q3TLX4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
DE   library, clone:G830026O06 product:lymphocyte protein tyrosine kinase,
DE   full insert sequence. (Fragment).
GN   Name=Lck;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
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RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK166263; BAE38668.1; -; mRNA.
DR   MGI; MGI:96756; Lck.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   368 AA;  42018 MW;  7AB6AE53AF1A5059 CRC64;

  Query Match             94.1%;  Score 48;  DB 2;  Length 368;
  Best Local Similarity   90.0%;  Pred. No. 2.9;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              |||||||:||
Db        347 DYLRSVLDDF 356


RESULT 11
Q4FZR6_RAT
ID   Q4FZR6_RAT     PRELIMINARY;   PRT;   379 AA.
AC   Q4FZR6;
DT   30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   30-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Lck_mapped protein (Fragment).
GN   Name=Lck_mapped;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
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CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC099218; AAH99218.1; -; mRNA.
DR   SMR; Q4FZR6; 2-379.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   379 AA;  43336 MW;  7CDEB573BAFB53AB CRC64;

  Query Match             94.1%;  Score 48;  DB 2;  Length 379;
  Best Local Similarity   90.0%;  Pred. No. 3;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
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Db        358 DYLRSVLDDF 367


RESULT 12
LCK_MOUSE
ID   LCK_MOUSE      STANDARD;      PRT;   508 AA.
AC   P06240; Q61794; Q61795; Q62320; Q91X65;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   25-OCT-2005, sequence version 3.
DT   07-MAR-2006, entry version 74.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).
GN   Name=Lck; Synonyms=Lsk-t;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;
RA   Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;
RT   "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and
RT   overexpressed in the murine T cell lymphoma LSTRA.";
RL   Cell 43:393-404(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86146842; PubMed=3081813;
RA   Voronova A.F., Sefton B.M.;
RT   "Expression of a new tyrosine protein kinase is stimulated by
RT   retrovirus promoter insertion.";
RL   Nature 319:682-685(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89096891; PubMed=2850479;
RA   Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT   "Structure of the murine lck gene and its rearrangement in a murine
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RT   lymphoma cell line.";
RL   Mol. Cell. Biol. 8:3058-3064(1988).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.
RX   MEDLINE=88142832; PubMed=3501824;
RA   Voronova A.F., Adler H.T., Sefton B.M.;
RT   "Two lck transcripts containing different 5' untranslated regions are
RT   present in T cells.";
RL   Mol. Cell. Biol. 7:4407-4413(1987).
RN   [7]
RP   MUTAGENESIS OF TYR-504.
RX   MEDLINE=88248001; PubMed=3380790;
RA   Amrein K.E., Sefton B.M.;
RT   "Avian reovirus mRNAs are nonfunctional in infected mouse cells:
RT   translational basis for virus host-range restriction.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).
RN   [8]
RP   INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19
RP   AND CYS-22.
RX   MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;
RA   Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,
RA   Littman D.R.;
RT   "Interaction of the unique N-terminal region of tyrosine kinase p56lck
RT   with cytoplasmic domains of CD4 and CD8 is mediated by cysteine
RT   motifs.";
RL   Cell 60:755-765(1990).
RN   [9]
RP   MUTAGENESIS.
RX   MEDLINE=93059694; PubMed=1279202;
RA   Hurley T.R., Amrein K.E., Sefton B.M.;
RT   "Creation and characterization of temperature-sensitive mutants of the
RT   lck tyrosine protein kinase.";
RL   J. Virol. 66:7406-7413(1992).
RN   [10]
RP   MUTAGENESIS OF LYS-272.
RX   MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;
RA   Abraham N., Miceli M.C., Parnes J.C., Veillette A.;
RT   "Enhancement of T-cell responsiveness by the lymphocyte-specific
RT   tyrosine protein kinase p56lck.";
RL   Nature 350:62-66(1991).
RN   [11]
RP   MUTAGENESIS OF TYR-504.
RX   MEDLINE=91219495; PubMed=1708890;
RA   Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;
RT   "Thymic tumorigenesis induced by overexpression of p56lck.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
RN   [12]
RP   PHOSPHORYLATION BY CSK.
RX   PubMed=8371758; DOI=10.1038/365156a0;
RA   Chow L.M., Fournel M., Davidson D., Veillette A.;
RT   "Negative regulation of T-cell receptor signalling by tyrosine protein
RT   kinase p50csk.";
RL   Nature 365:156-160(1993).
RN   [13]
RP   MUTAGENESIS.
RX   MEDLINE=93133805; PubMed=8421674;
RA   Carrera A.C., Alexandrov K., Roberts T.M.;
RT   "The conserved lysine of the catalytic domain of protein kinases is
RT   actively involved in the phosphotransfer reaction and not required for
RT   anchoring ATP.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
RN   [14]
RP   PALMITOYLATION.
RX   MEDLINE=94019312; PubMed=8413237;
RA   Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
RT   "Palmitylation of an amino-terminal cysteine motif of protein tyrosine
RT   kinases p56lck and p59fyn mediates interaction with glycosyl-
RT   phosphatidylinositol-anchored proteins.";
RL   Mol. Cell. Biol. 13:6385-6392(1993).
RN   [15]
RP   PALMITOYLATION.
RX   MEDLINE=95071286; PubMed=7980442;
RA   Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;
RT   "Palmitoylation of multiple Src-family kinases at a homologous N-
RT   terminal motif.";
RL   Biochem. J. 303:749-753(1994).
RN   [16]
RP   INTERACTION WITH CBLB.
RX   PubMed=10646608; DOI=10.1038/35003228;
RA   Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,
RA   Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,
RA   Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,
RA   Penninger J.M.;
RT   "Negative regulation of lymphocyte activation and autoimmunity by the
RT   molecular adaptor Cbl-b.";
RL   Nature 403:211-216(2000).
RN   [17]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [18]
RP   PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.
RX   PubMed=15592455; DOI=10.1038/nbt1046;
RA   Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA   Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT   "Immunoaffinity profiling of tyrosine phosphorylation in cancer

  Query Match             94.1%;  Score 48;  DB 1;  Length 508;
  Best Local Similarity   90.0%;  Pred. No. 4.1;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              |||||||:||
Db        487 DYLRSVLDDF 496


RESULT 13
Q4RNX3_TETNG
ID   Q4RNX3_TETNG   PRELIMINARY;   PRT;   466 AA.
AC   Q4RNX3;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Chromosome 10 SCAF15009, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00031368001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
```

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RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01015009; CAG09909.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase.
FT   NON_TER     466     466
SQ   SEQUENCE   466 AA;  53437 MW;  E35D93F87395B799 CRC64;

  Query Match             92.2%;  Score 47;  DB 2;  Length 466;
  Best Local Similarity   90.0%;  Pred. No. 5.7;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
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Db        448 EYLRSVLEDF 457


RESULT 14
O13064_XENLA
ID   O13064_XENLA   PRELIMINARY;   PRT;   488 AA.
AC   O13064;
DT   01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT   01-JUL-1997, sequence version 1.
DT   07-FEB-2006, entry version 29.
DE   Lyn protein tyrosine kinase.
GN   Name=Lyn;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fukami Y., Funabiki K., Sato K.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB003358; BAA20078.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; O13064; 43-488.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   488 AA;  55795 MW;  B7E70668B6EA92B2 CRC64;

  Query Match             86.3%;  Score 44;  DB 2;  Length 488;
  Best Local Similarity   80.0%;  Pred. No. 22;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
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Db        467 DYLQSVLDDF 476


RESULT 15
Q3U6Q5_MOUSE
ID   Q3U6Q5_MOUSE   PRELIMINARY;   PRT;   491 AA.
AC   Q3U6Q5;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830119M13 product:Yamaguchi sarcoma viral (v-yes-1) oncogene
DE   homolog, full insert sequence.
GN   Name=Lyn;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
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RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC ---

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DR EMBL; AK153038; BAE31669.1; -; mRNA.
DR MGI; MGI:96892; Lyn.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR GO; GO:0007242; P:intracellular signaling cascade; IDA.

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DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   491 AA;  56285 MW;  2C82015D510B1F59 CRC64;

  Query Match             86.3%;  Score 44;  DB 2;  Length 491;
  Best Local Similarity   80.0%;  Pred. No. 22;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              |||:|||:||
Db        470 DYLQSVLDDF 479


RESULT 16
Q8CEI0_MOUSE
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AC   Q8CEI0;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   10 day old male pancreas cDNA, RIKEN full-length enriched library,
DE   clone:1810073A02 product:Yamaguchi sarcoma viral (v-yes-1) oncogene
DE   homolog, full insert sequence.
GN   Name=Lyn;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
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RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK028112; BAC25753.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q8CEI0; 46-491.
DR   Ensembl; ENSMUSG00000042228; Mus musculus.
DR   MGI; MGI:96892; Lyn.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.

  Query Match             86.3%;  Score 44;  DB 2;  Length 491;
  Best Local Similarity   80.0%;  Pred. No. 22;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
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Db        470 DYLQSVLDDF 479


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DT   23-NOV-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Hypothetical protein.
GN   ORFNames=RCJMB04_2j8;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CB; TISSUE=Bursa;
RA   Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA   Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA   Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT   "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT   genefunction analysis.";
RL   Genome Biol. 6:R6-R6(2005).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ719465; CAG31124.1; -; mRNA.
DR   SMR; Q5ZMB9; 46-492.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
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DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   492 AA;  56202 MW;  69D2F0534E33CC1E CRC64;

  Query Match             86.3%;  Score 44;  DB 2;  Length 492;
  Best Local Similarity   80.0%;  Pred. No. 22;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
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Db        471 DYLQSVLDDF 480


RESULT 18
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AC   P07948;
DT   01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1994, sequence version 2.
DT   07-MAR-2006, entry version 74.
DE   Tyrosine-protein kinase Lyn (EC 2.7.1.112).
GN   Name=LYN;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87172710; PubMed=3561390;
RA   Yamanashi Y., Fukushige S., Semba K., Sukegawa J., Miyajima N.,
RA   Matsubara K., Yamamoto T., Toyoshima K.;
RT   "The yes-related cellular gene lyn encodes a possible tyrosine kinase
RT   similar to p56lck.";
RL   Mol. Cell. Biol. 7:237-243(1987).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=94171041; PubMed=8125304; DOI=10.1016/0378-1119(94)90811-7;
RA   Rider L.G., Raben N., Miller L., Jelsema C.;
RT   "The cDNAs encoding two forms of the LYN protein tyrosine kinase are
RT   expressed in rat mast cells and human myeloid cells.";
RL   Gene 138:219-222(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LYN A).
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 368-423.
RX   MEDLINE=91062389; PubMed=2247464;
RA   Partanen J., Maekelae T.P., Alitalo R., Lehvaeslaiho H., Alitalo K.;
RT   "Putative tyrosine kinases expressed in K-562 human leukemia cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917(1990).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 368-423.
RX   MEDLINE=92378604; PubMed=1510669;
RA   Bielke W., Ziemieki A., Kappos L., Miescher G.C.;
RT   "Expression of the B cell-associated tyrosine kinase gene Lyn in
RT   primary neuroblastoma tumours and its modulation during the
RT   differentiation of neuroblastoma cell lines.";
RL   Biochem. Biophys. Res. Commun. 186:1403-1409(1992).
RN   [6]
RP   INTERACTION WITH EPSTEIN-BARR VIRUS LMP2A.
RX   PubMed=7895172;
RA   Miller C.L., Burkhardt A.L., Lee J.H., Stealey B., Longnecker R.,
RA   Bolen J.B., Kieff E.;
RT   "Integral membrane protein 2 of Epstein-Barr virus regulates
RT   reactivation from latency through dominant negative effects on
RT   protein-tyrosine kinases.";
RL   Immunity 2:155-166(1995).
RN   [7]
RP   PHOSPHORYLATION SITE TYR-507, AND MASS SPECTROMETRY.
RX   PubMed=15592455; DOI=10.1038/nbt1046;
RA   Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA   Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT   "Immunoaffinity profiling of tyrosine phosphorylation in cancer
RT   cells.";
RL   Nat. Biotechnol. 23:94-101(2005).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.
CC       Interacts with Epstein-Barr virus LMP2A.
CC   -!- INTERACTION:
CC       O92969:- (xeno); NbExp=2; IntAct=EBI-79452, EBI-710506;
CC       P26660:- (xeno); NbExp=1; IntAct=EBI-79452, EBI-706322;
CC       P27958:- (xeno); NbExp=5; IntAct=EBI-79452, EBI-706378;
CC       Q9WMX2:- (xeno); NbExp=2; IntAct=EBI-79452, EBI-710918;
CC       P20273:CD22; NbExp=1; IntAct=EBI-79452, EBI-78277;
CC       Q6NVF1:Centd3 (xeno); NbExp=2; IntAct=EBI-79452, EBI-621463;
CC       P67870:CSNK2B; NbExp=1; IntAct=EBI-79452, EBI-348169;
CC       Q9UIF2:gpVI; NbExp=2; IntAct=EBI-79452, EBI-515278;
CC       Q07666:KHDRBS1; NbExp=1; IntAct=EBI-79452, EBI-1364;
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LYN A;
CC         IsoId=P07948-1; Sequence=Displayed;
CC       Name=LYN B;
CC         IsoId=P07948-2; Sequence=VSP_005002;
CC   -!- TISSUE SPECIFICITY: Expressed in primary neuroblastoma tumors.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; M16038; AAA59540.1; -; mRNA.
DR   EMBL; M79321; AAB50019.1; -; mRNA.
DR   EMBL; BC075001; AAH75001.1; -; mRNA.
DR   EMBL; BC075002; AAH75002.1; -; mRNA.
DR   PIR; A26719; TVHULY.
DR   PDB; 1W1F; NMR; A=60-122.
DR   PDB; 1WA7; NMR; A=60-122.
DR   SMR; P07948; 66-511.
DR   IntAct; P07948; -.
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DR   Ensembl; ENSG00000147507; Homo sapiens.
DR   HGNC; HGNC:6735; LYN.
DR   MIM; 165120; gene.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . .; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   3D-structure; Alternative splicing; ATP-binding; Kinase; Lipoprotein;
KW   Myristate; Nucleotide-binding; Palmitate; Phosphorylation;
KW   Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    511       Tyrosine-protein kinase Lyn.
FT                                /FTId=PRO_0000088129.
FT   DOMAIN       62    122       SH3.
FT   DOMAIN      128    225       SH2.
FT   DOMAIN      246    500       Protein kinase.
FT   NP_BIND     252    260       ATP (By similarity).
FT   ACT_SITE    366    366       Proton acceptor (By similarity).
FT   BINDING     274    274       ATP (By similarity).
FT   MOD_RES     396    396       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     507    507       Phosphotyrosine.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   VARSPLIC     22     42       Missing (in isoform LYN B).
FT                                /FTId=VSP_005002.
FT   STRAND       65     71
FT   STRAND       73     73
FT   STRAND       77     79
FT   STRAND       83     83
FT   TURN         85     86
FT   STRAND       88     94
FT   STRAND       96    103
FT   TURN        104    106
FT   STRAND      109    113
FT   TURN        114    116
FT   STRAND      117    119
SQ   SEQUENCE   511 AA;  58443 MW;  8419CD461204E364 CRC64;

  Query Match             86.3%;  Score 44;  DB 1;  Length 511;
  Best Local Similarity   80.0%;  Pred. No. 23;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
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Db        490 DYLQSVLDDF 499


RESULT 19
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LYN_MOUSE
ID   LYN_MOUSE      STANDARD;      PRT;   511 AA.
AC   P25911; Q62127;
DT   01-MAY-1992, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1997, sequence version 3.
DT   07-MAR-2006, entry version 64.
DE   Tyrosine-protein kinase Lyn (EC 2.7.1.112).
GN   Name=Lyn;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=91260688; PubMed=1710766;
RA   Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A., Lock P.,
RA   Dunn A.R.;
RT   "Alternatively spliced murine lyn mRNAs encode distinct proteins.";
RL   Mol. Cell. Biol. 11:3399-3406(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=91203857; PubMed=2017160;
RA   Yi T., Bolen J.B., Ihle J.N.;
RT   "Hematopoietic cells express two forms of lyn kinase differing by 21
RT   amino acids in the amino terminus.";
RL   Mol. Cell. Biol. 11:2391-2398(1991).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LYN A).
RC   STRAIN=Czech II; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 363-431.
RX   MEDLINE=90152381; PubMed=2482828; DOI=10.1016/0378-1119(89)90465-4;
RA   Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
RT   "The application of the polymerase chain reaction to cloning members
RT   of the protein tyrosine kinase family.";
RL   Gene 85:67-74(1989).
RN   [5]
RP   INTERACTION WITH LIME1.
RX   PubMed=16249387; DOI=10.1182/blood-2005-05-1859;
RA   Ahn E., Lee H., Yun Y.;
RT   "LIME acts as a transmembrane adapter mediating BCR-dependent B-cell
RT   activation.";
RL   Blood 107:1521-1527(2006).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LYN A;
CC         IsoId=P25911-1; Sequence=Displayed;
CC       Name=LYN B;
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CC         IsoId=P25911-2; Sequence=VSP_005003;
CC   -!- TISSUE SPECIFICITY: Expressed predominantly in B-lymphoid and
CC       myeloid cells.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; M64608; AAA39470.1; -; mRNA.
DR   EMBL; M57696; AAA39471.1; -; mRNA.
DR   EMBL; M57697; AAA39472.1; -; mRNA.
DR   EMBL; BC031547; AAH31547.1; -; mRNA.
DR   EMBL; M33426; AAA40017.1; -; mRNA.
DR   PIR; A39719; A39719.
DR   HSSP; P08631; 1AD5.
DR   SMR; P25911; 66-511.
DR   IntAct; P25911; -.
DR   Ensembl; ENSMUSG00000042228; Mus musculus.
DR   MGI; MGI:96892; Lyn.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR   GO; GO:0046777; P:autophosphorylation; IDA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Alternative splicing; ATP-binding; Kinase; Lipoprotein; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    511       Tyrosine-protein kinase Lyn.
FT                                /FTId=PRO_0000088130.
FT   DOMAIN       62    122       SH3.
FT   DOMAIN      128    225       SH2.
FT   DOMAIN      246    500       Protein kinase.
FT   NP_BIND     252    260       ATP (By similarity).
FT   ACT_SITE    366    366       Proton acceptor (By similarity).
FT   BINDING     274    274       ATP (By similarity).
FT   MOD_RES     396    396       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     507    507       Phosphotyrosine (By similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   VARSPLIC     24     44       Missing (in isoform LYN B).
FT                                /FTId=VSP_005003.
FT   CONFLICT     76     76       I -> F (in Ref. 2).
FT   CONFLICT    160    160       L -> I (in Ref. 2).
FT   CONFLICT    278    278       P -> L (in Ref. 2).
FT   CONFLICT    390    390       V -> I (in Ref. 2).
FT   CONFLICT    414    414       I -> F (in Ref. 4).
FT   CONFLICT    424    424       D -> N (in Ref. 1).
FT   CONFLICT    431    431       L -> P (in Ref. 4).
SQ   SEQUENCE   511 AA;  58681 MW;  3935221CC90C50F0 CRC64;

  Query Match             86.3%;  Score 44;  DB 1;  Length 511;
  Best Local Similarity   80.0%;  Pred. No. 23;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
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Db        490 DYLQSVLDDF 499


RESULT 20
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ID   LYN_RAT        STANDARD;      PRT;   511 AA.
AC   Q07014; Q63320;
DT   01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1997, sequence version 2.
DT   07-MAR-2006, entry version 57.
DE   Tyrosine-protein kinase Lyn (EC 2.7.1.112).
GN   Name=Lyn;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Minoguchi K., Nishikata H., Siraganian R.P.;
RT   "Bacterially expressed rat p56lyn binds several proteins in rat
RT   basophilic leukemia cells including pp72, a tyrosine phosphorylated
RT   protein prominent in activated cells.";
RL   J. Immunol. 150:222-222(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=94171041; PubMed=8125304; DOI=10.1016/0378-1119(94)90811-7;
RA   Rider L.G., Raben N., Miller L., Jelsema C.;
RT   "The cDNAs encoding two forms of the LYN protein tyrosine kinase are
RT   expressed in rat mast cells and human myeloid cells.";
RL   Gene 138:219-222(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=97442484; PubMed=9295361; DOI=10.1074/jbc.272.38.24072;
RA   Vonakis B.M., Chen H., Haleem-Smith H., Metzger H.;
RT   "The unique domain as the site on Lyn kinase for its constitutive
RT   association with the high affinity receptor for IgE.";
RL   J. Biol. Chem. 272:24072-24080(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LYN A;
CC         IsoId=Q07014-1; Sequence=Displayed;
CC       Name=LYN B;
CC         IsoId=Q07014-2; Sequence=VSP_005004;
CC   -!- TISSUE SPECIFICITY: Expressed predominantly in B-lymphoid and
CC       myeloid cells.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; L14951; AAA41549.1; -; mRNA.
DR   EMBL; L14782; AAA20944.1; -; mRNA.
DR   EMBL; L14823; AAA20945.1; -; mRNA.
DR   EMBL; AF000300; AAB71344.1; -; mRNA.
DR   EMBL; AF000301; AAB71345.1; -; mRNA.
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DR   EMBL; AF000302; AAB71346.1; -; mRNA.
DR   PIR; I56160; I56160.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q07014; 66-511.
DR   Ensembl; ENSRNOG00000008180; Rattus norvegicus.
DR   RGD; 621017; Lyn.
DR   GO; GO:0016301; F:kinase activity; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Alternative splicing; ATP-binding; Kinase; Lipoprotein; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    511       Tyrosine-protein kinase Lyn.
FT                                /FTId=PRO_0000088131.
FT   DOMAIN       62    122       SH3.
FT   DOMAIN      128    225       SH2.
FT   DOMAIN      246    500       Protein kinase.
FT   NP_BIND     252    260       ATP (By similarity).
FT   ACT_SITE    366    366       Proton acceptor (By similarity).
FT   BINDING     274    274       ATP (By similarity).
FT   MOD_RES     396    396       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     507    507       Phosphotyrosine (By similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   VARSPLIC     24     44       Missing (in isoform LYN B).
FT                                /FTId=VSP_005004.
FT   CONFLICT    230    230       P -> L (in Ref. 2).
FT   CONFLICT    307    307       V -> A (in Ref. 2).
FT   CONFLICT    418    418       C -> Y (in Ref. 2).
SQ   SEQUENCE   511 AA;  58529 MW;  24A2E5E229CD43ED CRC64;

  Query Match             86.3%;  Score 44;  DB 1;  Length 511;
  Best Local Similarity   80.0%;  Pred. No. 23;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              |||:|||:||
Db        490 DYLQSVLDDF 499


RESULT 21
Q3TCS3_MOUSE
ID   Q3TCS3_MOUSE   PRELIMINARY;   PRT;   512 AA.
AC   Q3TCS3;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched
DE   library, clone:F630107O15 product:Yamaguchi sarcoma viral (v-yes-1)
DE   oncogene homolog, full insert sequence (Bone marrow macrophage cDNA,
DE   RIKEN full-length enriched library, clone:I830054M12 product:Yamaguchi
DE   sarcoma viral (v-yes-1) oncogene homolog, full insert sequence).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK170561; BAE41882.1; -; mRNA.
DR   EMBL; AK152199; BAE31028.1; -; mRNA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.

  Query Match             86.3%;  Score 44;  DB 2;  Length 512;
  Best Local Similarity   80.0%;  Pred. No. 23;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              |||:|||:||
Db        491 DYLQSVLDDF 500


RESULT 22
Q6NUK7_HUMAN
ID   Q6NUK7_HUMAN   PRELIMINARY;   PRT;   582 AA.
AC   Q6NUK7;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   LYN protein (Fragment).
GN   Name=LYN;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
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RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May serve as part of a signaling pathway coupling the Fc
CC       receptor to the activation of the respiratory burst. May also
CC       contribute to neutrophil migration and may regulate the
CC       degranulation process of neutrophils (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC068551; AAH68551.1; -; mRNA.
DR   EMBL; BC059394; AAH59394.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q6NUK7; 24-86, 137-582.
DR   Ensembl; ENSG00000147507; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000108; Neu_cyt_fact_2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00499; P67PHOX.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   582 AA;  65809 MW;  1CFF99768C28E9BB CRC64;

  Query Match             86.3%;  Score 44;  DB 2;  Length 582;
  Best Local Similarity   80.0%;  Pred. No. 27;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
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Db        561 DYLQSVLDDF 570


RESULT 23
Q9DDK6_SALSA
ID   Q9DDK6_SALSA   PRELIMINARY;   PRT;   502 AA.
AC   Q9DDK6;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 20.
DE   Src-family tyrosine kinase SCK.
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hordvik I., Male R.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF321110; AAG38611.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q9DDK6; 54-502.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   502 AA;  56600 MW;  82DF0D677AA99980 CRC64;
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  Query Match             84.3%;  Score 43;  DB 2;  Length 502;
  Best Local Similarity   80.0%;  Pred. No. 35;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              :||:||||||
Db        481 EYLQSVLEDF 490


RESULT 24
Q6TPQ4_BRARE
ID   Q6TPQ4_BRARE   PRELIMINARY;   PRT;   503 AA.
AC   Q6TPQ4;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Lymphocyte protein tyrosine kinase.
GN   Name=lck;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   PubMed=15123839; DOI=10.1073/pnas.0402248101;
RA   Langenau D.M., Ferrando A.A., Traver D., Kutok J.L., Hezel J.P.,
RA   Kanki J.P., Zon L.I., Look A.T., Trede N.S.;
RT   "In vivo tracking of T cell development, ablation, and engraftment in
RT   transgenic zebrafish.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:7369-7374(2004).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY390224; AAR26383.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   ZFIN; ZDB-GENE-040617-1; lck.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   503 AA;  57504 MW;  F011D1B9BDC63C1C CRC64;

  Query Match             84.3%;  Score 43;  DB 2;  Length 503;
  Best Local Similarity   80.0%;  Pred. No. 35;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ::||||||||
Db        481 EFLRSVLEDF 490


RESULT 25
O93411_XENLA
ID   O93411_XENLA   PRELIMINARY;   PRT;   496 AA.
AC   O93411;
DT   01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1998, sequence version 1.
DT   07-FEB-2006, entry version 25.
DE   Non-receptor protein tyrosine kinase laloo.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Weinstein D.C., Marden J., Carnevali F., Hemmati-Brivanlou A.;
RT   "FGF-mediated mesoderm induction involves the Src-family kinase
RT   laloo.";
RL   Nature 0:0-0(1998).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF081803; AAC31209.1; -; mRNA.
DR   HSSP; P06239; 1QPC.
DR   SMR; O93411; 54-496.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase; Receptor.
SQ   SEQUENCE   496 AA;  56275 MW;  96223A6F99689965 CRC64;

  Query Match             82.4%;  Score 42;  DB 2;  Length 496;
  Best Local Similarity   70.0%;  Pred. No. 53;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              :||:|:||||
Db        475 EYLQSILEDF 484


RESULT 26
LCK_CHICK
```

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ID   LCK_CHICK      STANDARD;      PRT;   507 AA.
AC   P42683; Q53WS8;
DT   01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1995, sequence version 1.
DT   07-MAR-2006, entry version 47.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-
DE   tyrosine kinase C-TKL) (p56tkl).
GN   Name=LCK;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Spleen;
RA   Gaertner T., Khnel H., Strebhardt K., Ruebsamen-Waigmann H.;
RL   Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 1-88.
RX   MEDLINE=92186854; PubMed=1545804;
RA   Chow L., Ratcliffe M., Veillette A.;
RT   "tkl is the avian homolog of the mammalian lck tyrosine protein kinase
RT   gene.";
RL   Mol. Cell. Biol. 12:1226-1233(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 46-507.
RX   MEDLINE=88097370; PubMed=3321053;
RA   Strebhardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.;
RT   "Additional member of the protein-tyrosine kinase family: the src- and
RT   lck-related protooncogene c-tkl.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD4, CD8 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Bound to the cytoplasmic domain of either
CC       CD4 or CD8 (By similarity).
CC   -!- PTM: Phosphorylated on Tyr-503. This phosphorylation downregulates
CC       catalytic activity. Phosphorylated on Tyr-392 either by itself or
CC       another kinase, leading to increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
DR   EMBL; X60380; CAA42930.1; -; mRNA.
DR   EMBL; M85043; AAA49003.1; -; mRNA.
DR   EMBL; J03579; AAA49081.1; ALT_INIT; mRNA.
DR   HSSP; P06239; 3LCK.
DR   SMR; P42683; 63-507.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    507       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088128.
FT   DOMAIN       59    119       SH3.
FT   DOMAIN      125    222       SH2.
FT   DOMAIN      243    496       Protein kinase.
FT   NP_BIND     249    257       ATP (By similarity).
FT   ACT_SITE    362    362       Proton acceptor (By similarity).
FT   BINDING     271    271       ATP (By similarity).
FT   MOD_RES     392    392       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     503    503       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   507 AA;  58009 MW;  BC83C4FA891B6170 CRC64;

  Query Match             82.4%;  Score 42;  DB 1;  Length 507;
  Best Local Similarity   70.0%;  Pred. No. 54;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              :|::||||||
Db        486 EYMKSVLEDF 495


RESULT 27
Q66I04_BRARE
ID   Q66I04_BRARE   PRELIMINARY;   PRT;   510 AA.
AC   Q66I04;
DT   11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Zgc:92124.
GN   ORFNames=zgc:92124;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
```

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RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC081601; AAH81601.1; -; mRNA.
DR   SMR; Q66I04; 65-510.
DR   Ensembl; ENSDARG00000031715; Danio rerio.
DR   ZFIN; ZDB-GENE-040912-7; zgc:92124.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   510 AA;  58258 MW;  5EE8F68226569BA2 CRC64;

  Query Match            82.4%;  Score 42;  DB 2;  Length 510;
  Best Local Similarity  70.0%;  Pred. No. 55;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLEDF 10
              ||::|||:||
Db        489 DYIQSVLDDF 498


RESULT 28
Q5RHX5_BRARE
ID   Q5RHX5_BRARE   PRELIMINARY;   PRT;   196 AA.
AC   Q5RHX5;
DT   21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   21-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Novel protein.
GN   Name=si:ch211-14g4.1; Synonyms=OTTDARP00000006609;
GN   ORFNames=CH211-14G4.1-002;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gray E.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BX323889; CAI11617.1; -; Genomic_DNA.
DR   ZFIN; ZDB-GENE-041014-248; si:ch211-14g4.1.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR005176; DUF298.
DR   InterPro; IPR011992; EF-Hand_type.
DR   PANTHER; PTHR12281; DUF298; 1.
DR   Pfam; PF03556; DUF298; 1.
KW   Repeat.
SQ   SEQUENCE   196 AA;  22988 MW;  C0061C1D51E3CCC2 CRC64;

  Query Match            78.4%;  Score 40;  DB 2;  Length 196;
  Best Local Similarity  88.9%;  Pred. No. 47;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLED 9
              ||||||| |
Db        120 DYLRSVLND 128


RESULT 29
DCNL4_BRARE
ID   DCNL4_BRARE    STANDARD;      PRT;   280 AA.
AC   Q5RHX6;
DT   25-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT   25-OCT-2005, sequence version 2.
DT   07-MAR-2006, entry version 9.
DE   DCN1-like protein 4 (Defective in cullin neddylation protein 1-like
DE   protein 4) (DCUN1 domain-containing protein 4).
GN   Name=dcun1d4; Synonyms=si:ch211-14g4.1;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   The Danio rerio sequencing project at the Sanger Institute;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 DCUN1 domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BX323889; CAI11616.1; ALT_INIT; Genomic_DNA.
DR   ZFIN; ZDB-GENE-041014-248; si:ch211-14g4.1.
DR   InterPro; IPR005176; DUF298.
DR   Pfam; PF03556; DUF298; 1.
FT   CHAIN         1    280       DCN1-like protein 4.
FT                                /FTId=PRO_0000129505.
FT   DOMAIN      161    275       DCUN1.
SQ   SEQUENCE   280 AA;  32421 MW;  A0C354AACC15688C CRC64;

  Query Match            78.4%;  Score 40;  DB 1;  Length 280;
  Best Local Similarity  88.9%;  Pred. No. 69;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLED 9
              ||||||| |
Db        169 DYLRSVLND 177


RESULT 30
Q4RKU7_TETNG
ID   Q4RKU7_TETNG   PRELIMINARY;   PRT;   281 AA.
AC   Q4RKU7;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
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DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Chromosome 1 SCAF15025, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00032781001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01015025; CAG10985.1; -; Genomic_DNA.
DR   InterPro; IPR005176; DUF298.
DR   PANTHER; PTHR12281; DUF298; 1.
DR   Pfam; PF03556; DUF298; 1.
FT   NON_TER       1      1
FT   NON_TER     281    281
SQ   SEQUENCE   281 AA;  32851 MW;  35EDC7C4ED12D8C9 CRC64;

  Query Match             78.4%;  Score 40;  DB 2;  Length 281;
  Best Local Similarity   88.9%;  Pred. No. 69;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DYLRSVLED 9
              ||||||| |
Db        170 DYLRSVLND 178


Search completed: June 29, 2006, 09:29:42
Job time : 120.701 secs
```

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 87.8313 Seconds
(without alignments)
46.851 Million cell updates/sec

Title: US-10-062-257A-3
Perfect score: 50
Sequence: 1 HYTNASDGL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	9	4	AAB73119	Aab73119 Tumour an
2	50	100.0	9	6	ABR84375	Abr84375 Human lck
3	50	100.0	9	8	ADS87116	Ads87116 Human gen
4	50	100.0	9	9	ADX58315	Adx58315 Partial a
5	50	100.0	9	9	ADZ42230	Adz42230 Cytotoxic
6	50	100.0	9	9	AEC33131	Aec33131 Lck tumor
7	50	100.0	9	10	AEE99213	Aee99213 Cancer an
8	50	100.0	98	7	ADN11799	Adn11799 Lck SH2 d
9	50	100.0	101	2	AAW31184	Aaw31184 Human p56
10	50	100.0	102	2	AAR60992	Aar60992 Fragment
11	50	100.0	102	2	AAR72090	Aar72090 Lck SH2 r
12	50	100.0	134	2	AAW03982	Aaw03982 DET1-DET2
13	50	100.0	134	2	AAW02120	Aaw02120 DET1-DET2
14	50	100.0	134	2	AAW11286	Aaw11286 DET1-DET2
15	50	100.0	134	2	AAW19624	Aaw19624 Human lck
16	50	100.0	224	2	AAW14788	Aaw14788 FKBP-LCK:
17	50	100.0	224	2	AAW96823	Aaw96823 A fusion
18	50	100.0	363	6	ABR59690	Abr59690 Human p56
19	50	100.0	363	8	ADP48375	Adp48375 Human lym
20	50	100.0	437	5	ABG79672	Abg79672 Tumour in
21	50	100.0	508	3	AAB37700	Aab37700 Human lym
22	50	100.0	508	7	ADE58802	Ade58802 Human Pro
23	50	100.0	508	7	ADE58799	Ade58799 Human Pro
24	50	100.0	508	7	ADF45072	Adf45072 Human kin
25	50	100.0	508	7	ADL34479	Adl34479 Human lym
26	50	100.0	508	8	ADS88148	Ads88148 Human pro
27	50	100.0	509	3	AAY49420	Aay49420 PKA subst
28	50	100.0	509	6	ABR58699	Abr58699 Human can
29	50	100.0	509	7	ABR56202	Abr56202 Human Lym
30	50	100.0	509	7	ADE40449	Ade40449 Human pro
31	50	100.0	509	8	ADL22907	Adl22907 Human MP2
32	50	100.0	509	8	ADP12458	Adp12458 Protein e
33	50	100.0	509	8	ADP48374	Adp48374 Human lym
34	50	100.0	509	9	ADZ51107	Adz51107 Amino aci
35	50	100.0	509	9	AEA35921	Aea35921 Human Lck
36	50	100.0	539	8	ABM82981	Abm82981 Human dia
37	50	100.0	539	8	ABM82982	Abm82982 Human dia
38	50	100.0	567	5	ABG79673	Abg79673 Tumour in
39	40	80.0	12	2	AAR63397	Aar63397 Peptide f
40	40	80.0	193	2	AAR63367	Aar63367 Hepatitis
41	40	80.0	298	2	AAR84183	Aar84183 Megakaryo
42	40	80.0	505	2	AAR41941	Aar41941 pTK gene
43	40	80.0	505	2	AAR85929	Aar85929 Protein t
44	40	80.0	505	6	ABU70942	Abu70942 Human adi
45	40	80.0	505	6	ABU08943	Abu08943 Human nuc
46	40	80.0	505	6	ABU08944	Abu08944 Human nuc
47	40	80.0	505	6	ABU08941	Abu08941 Human nuc
48	37	74.0	382	8	ADS26708	Ads26708 Bacterial
49	37	74.0	382	8	ADS27093	Ads27093 Bacterial
50	37	74.0	382	8	ADS26341	Ads26341 Bacterial
51	37	74.0	660	8	ADN25600	Adn25600 Bacterial
52	36	72.0	16	9	AEA15030	Aea15030 pTRG Lox
53	36	72.0	226	5	ABG95124	Abg95124 Human c-s
54	36	72.0	298	8	ADR39735	Adr39735 Human kin
55	36	72.0	345	2	AAR52824	Aar52824 GTP-cyclo
56	36	72.0	357	5	AAU78677	Aau78677 Human SH2
57	36	72.0	450	3	AAY49418	Aay49418 PKA subst
58	36	72.0	450	3	AAY44448	Aay44448 Wild-type
59	36	72.0	450	4	AAG67623	Aag67623 Amino aci
60	36	72.0	450	4	AAB84662	Aab84662 Amino aci
61	36	72.0	450	4	AAG67444	Aag67444 Amino aci
62	36	72.0	450	6	ABR47428	Abr47428 Breast ca
63	36	72.0	450	6	ABR59696	Abr59696 Human c-s
64	36	72.0	450	6	ABO07208	Abo07208 Human p53
65	36	72.0	450	6	ADA00841	Ada00841 Human Src
66	36	72.0	450	7	ADE63739	Ade63739 Human Pro
67	36	72.0	450	7	ADF45046	Adf45046 Human kin
68	36	72.0	450	8	ADO51277	Ado51277 Human c-s
69	36	72.0	450	8	ADS88151	Ads88151 Human pro
70	36	72.0	450	9	AED01120	Aed01120 Human c-S
71	36	72.0	459	4	AAO13873	Aao13873 Human pol
72	36	72.0	459	9	AEA20969	Aea20969 Novel hum
73	36	72.0	463	7	ADL57015	Adl57015 Csk. 5/20
74	36	72.0	463	9	AEA20073	Aea20073 Novel hum
75	36	72.0	476	8	ABM84178	Abm84178 Human dia
76	36	72.0	485	8	ABM84181	Abm84181 Human dia
77	36	72.0	485	8	ABM84179	Abm84179 Human dia
78	36	72.0	505	4	ABB71008	Abb71008 Drosophil
79	36	72.0	511	8	ABM84182	Abm84182 Human dia
80	36	72.0	511	8	ABM84180	Abm84180 Human dia
81	35	70.0	97	7	ADN11796	Adn11796 c-Yes SH2
82	35	70.0	104	2	AAY06343	Aay06343 Streptomy
83	35	70.0	179	4	ABG30013	Abg30013 Novel hum
84	35	70.0	197	6	ABP68430	Abp68430 Human col
85	35	70.0	230	4	ABG30014	Abg30014 Novel hum
86	35	70.0	263	2	AAR47235	Aar47235 Rubella E
87	35	70.0	330	4	ABG26073	Abg26073 Novel hum
88	35	70.0	381	2	AAY06368	Aay06368 Streptomy
89	35	70.0	381	3	AAB14881	Aab14881 Rhodother
90	35	70.0	381	5	AAU77589	Aau77589 S. livida
91	35	70.0	381	5	AAU77433	Aau77433 Streptomy
92	35	70.0	402	4	AAB85589	Aab85589 Wheat gly
93	35	70.0	402	5	ABP53636	Abp53636 Wheat gly
94	35	70.0	429	3	AAY84346	Aay84346 Amino aci
95	35	70.0	450	7	ADE63737	Ade63737 Rat Prote
96	35	70.0	450	9	ADW11847	Adw11847 Src kinas

97	35	70.0	451	7	ADD46393	Add46393 Rat Prote
98	35	70.0	498	7	ADF05197	Adf05197 Bacterial
99	35	70.0	499	8	ABM84206	Abm84206 Human dia
100	35	70.0	543	2	AAY24421	Aay24421 Human yes

ALIGNMENTS

RESULT 1
AAB73119
ID AAB73119 standard; peptide; 9 AA.
XX
AC AAB73119;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #3.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 1; Page 66; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 1 HYTNASDGL 9

RESULT 2
ABR84375
ID ABR84375 standard; peptide; 9 AA.
XX
AC ABR84375;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human lck HLA-A24 epitope, SEQ ID NO:25.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 8; Page 10; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 1 HYTNASDGL 9

RESULT 3
ADS87116
ID ADS87116 standard; peptide; 9 AA.
XX
AC ADS87116;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genetic vaccine/ubiquitin (Ub)/Lck-related epitope peptide 1.
XX
KW vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
KW colon; bladder; breast; oesophagus; kidney; brain; human; epitope; Lck.
XX
OS Homo sapiens.
XX
PN WO2004035085-A1.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-JP013279.
XX
PR 17-OCT-2002; 2002JP-00302816.
XX
PA (KYUS-) KYUSHU TLO CO LTD.
XX

PI Himeno K, Furue M, Maehara Y;
XX
DR WPI; 2004-357144/33.
XX
PT Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
PT or cytokine genes for prevention and treatment of cancer.
XX
PS Disclosure; SEQ ID NO 132; 266pp; Japanese.
XX
CC The invention relates to a novel genetic vaccine containing the ubiquitin
CC gene together with a gene encoding an antigenic protein containing a T-
CC cell target sequence. The vaccine of the invention may be useful for
CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma
CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence
CC is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide
CC of the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 1 HYTNASDGL 9

RESULT 4
ADX58315
ID ADX58315 standard; peptide; 9 AA.
XX
AC ADX58315;
XX
DT 21-APR-2005 (first entry)
XX
DE Partial antigenic peptide #1 derived from p56.
XX
KW cytostatic; vaccine; hematopoietic tumor; p56; immunotherapy.
XX
OS Unidentified.
XX
PN WO2005011723-A1.
XX
PD 10-FEB-2005.
XX
PF 05-AUG-2004; 2004WO-JP011232.
XX
PR 05-AUG-2003; 2003JP-00287208.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2005-152358/16.
XX
PT Prevention and/or therapeutic agent of hematopoietic tumor useful for
PT preventing and/or treating hematopoietic tumor, has peptides having amino
PT acid sequences of partial peptide of p56lck, SART-1, SART-2, SART-3, or
PT ART-1 protein.
XX
PS Claim 1; SEQ ID NO 1; 41pp; Japanese.
XX
CC The specification describes a remedy for a hematopoietic tumor. The
CC remedy comprises one or more peptides derived from p56 (lck), SART-1,
CC SART-2, SART-3, or ART-1 proteins as an active ingredient. The peptides
CC induce specific cytotoxic T cells. The remedy of thr invention is useful
CC for preventing and treating hematopoietic tumors comprising human
CC leukocyte antigen (HLA)-A24 molecules on its cell surface. It is also
CC useful in immunotherapy of hematopoietic tumors, and for treating
CC malignant tumors such as acute myelogenous leukemia, acute lymphoblastic
CC leukemia, chronic lymphocytic leukemia, malignant lymphoma, multiple
CC myeloma, etc. . The present sequence represents a partial peptide derived
CC from p56, and is used in the remedy of the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 1 HYTNASDGL 9

RESULT 5
ADZ42230
ID ADZ42230 standard; peptide; 9 AA.
XX
AC ADZ42230;
XX
DT 30-JUN-2005 (first entry)
XX
DE Cytotoxic T-lymphocyte epitope peptide, Lck-208.
XX
KW antibody; vaccine; immune stimulation; cytotoxic T-lymphocyte.
XX
OS Synthetic.
XX
PN JP2005099001-A.
XX
PD 14-APR-2005.
XX
PF 20-AUG-2004; 2004JP-00240269.
XX
PR 31-AUG-2003; 2003JP-00348853.
XX
PA (ITOK/) ITO K.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
XX
DR WPI; 2005-310369/32.
XX
PT Measuring anti-peptide antibody, by preparing supports immobilized with
PT different peptides, pouring test substance comprising peptide recognizing
PT antibody on supports, adding labeled secondary antibody, measuring amount
PT of label.
XX
PS Example 1; SEQ ID NO 6; 22pp; Japanese.
XX
CC The invention relates to a novel method for measuring an anti-peptide
CC antibody. The method involves preparing several supports immobilized with
CC different kinds of peptides, pouring a test substance comprising a
CC peptide recognizing antibody onto prepared supports for reacting a
CC peptide with an antibody, combining the peptide recognizing antibody with
CC a labeled secondary antibody, measuring the amount of coupled label and
CC identifying the kind of support for measuring the anti-peptide antibody.
CC The invention further comprises a method for selecting a peptide vaccine
CC candidate. The method enables the measurement of anti-peptide antibodies
CC from trace amounts of a sample, e.g. blood serum from patients, rapidly
CC with high efficiency. The immune response specific to a peptide vaccine
CC can be monitored efficiently. This sequence represents a cytotoxic T-
CC lymphocyte (CTL) epitope peptide of the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 1 HYTNASDGL 9

```
RESULT 6
AEC33131
ID   AEC33131 standard; peptide; 9 AA.
XX
AC   AEC33131;
XX
DT   17-NOV-2005  (first entry)
XX
DE   Lck tumor antigen peptide SEQ ID NO 6.
XX
KW   cytostatic; vaccine; gene therapy; epitope; immunogenicity; diagnosis;
KW   tumor-associated antigen; cancer; neoplasm; Lck.
XX
OS   Homo sapiens.
XX
PN   WO2005083074-A1.
XX
PD   09-SEP-2005.
XX
PF   01-MAR-2005; 2005WO-JP003399.
XX
PR   01-MAR-2004; 2004JP-00056865.
XX
PA   (UYKA-) UNIV KANAZAWA TECHNOLOGY LICENSING ORG.
XX
PI   Kaneko S,  Mizukoshi E,  Nakamoto Y,  Tsuji H;
XX
DR   WPI; 2005-619189/63.
XX
PT   Novel tumor antigen peptide derived from Cyp-B, SART, p53, alpha-
PT   fetoprotein and human telomerase reverse transcriptase, useful for
PT   preparing anti-tumor peptide vaccine.
XX
PS   Example 1; SEQ ID NO 6; 58pp; Japanese.
XX
CC   The invention describes a tumor antigen peptide (I) including Cyp-B,
CC   SART, p53, multidrug resistance protein (MRP), alpha-fetoprotein (AFP) or
CC   human telomerase reverse transcriptase (hTERT) derived peptide comprising
CC   an amino acid sequence (S1) of SEQ ID No. 4, 14, 15, 18, 19, 23-25, 27-
CC   30, 34, 37-41 or 44. Also described are: an anti-tumor peptide vaccine
CC   comprising (I); antigen presenting cells (II) presenting (I), obtained by
CC   cultivating human leukocyte antigen (HLA)-A24 positive antigen presenting
CC   cells with (I); nucleic acid molecule (III) comprising a base sequence
CC   encoding (S1); an antibody (A1) capable of specifically binding to (I);
CC   inducing (M1) cytotoxic T cells, involves cultivating tumor tissue
CC   infiltrated lymphocyte or peripheral blood lymphocyte isolated from the
CC   HLA-A24 positive patient, with (I) and interleukin (IL)-2; and anti-tumor
CC   agent comprising (III) or the cytotoxic T cell acquired by (M1). (I) is
CC   useful for preparing anti-tumor peptide vaccine. The nucleic acid
CC   molecule is useful as an anti-tumor agent. The antibody is useful for
CC   detecting or diagnosing cancer. (I) is an effective immunogenic peptide
CC   with respect to tumor. This is the amino acid sequence of a Lck tumor
CC   antigen peptide. Note: This sequence is also available in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 50;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db          1 HYTNASDGL 9


RESULT 7
AEE99213
ID   AEE99213 standard; peptide; 9 AA.
XX
AC   AEE99213;
XX
DT   23-FEB-2006  (first entry)
XX
DE   Cancer antigen lck peptide SEQ ID NO 3.
XX
KW   Cytostatic; Vaccine; cancer; neoplasm; antigen; lck.
XX
OS   Unidentified.
XX
PN   WO2005123122-A1.
XX
PD   29-DEC-2005.
XX
PF   21-JUN-2005; 2005WO-JP011357.
XX
PR   21-JUN-2004; 2004JP-00182811.
XX
PA   (UYKU-) UNIV KURUME.
XX
PI   Itoh K;
XX
DR   WPI; 2006-057212/06.
XX
PT   Treating cancer by evaluating specific cytotoxic T-lymphocyte precursors
PT   for each peptide of cancer antigen peptide set, in patient, administering
PT   peptide set obtained after removing peptide being non-specific to
PT   precursors, to patient.
XX
PS   Example 1; SEQ ID NO 3; 36pp; Japanese.
XX
CC   The invention relates to a method of treating a cancer patient by
CC   administering cancer antigens to patient, involves evaluating presence or
CC   absence of specific cytotoxic T-lymphocyte precursors for individual
CC   peptides contained in set of cancer antigen peptides, in patient,
CC   removing peptide being non-specific to precursors, from cancer antigen
CC   peptide set, to prepare set for administration, and administering cancer
CC   antigen peptide set to patient. The method is useful for treating cancer
CC   patient by administering cancer antigens to patient. The present sequence
CC   represents the amino acid sequence of a lck peptide cancer antigen.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 50;  DB 10;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db          1 HYTNASDGL 9


RESULT 8
ADN11799
ID   ADN11799 standard; protein; 98 AA.
XX
AC   ADN11799;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Lck SH2 domain, SEQ ID 5.
XX
KW   Cytostatic; SH2-phosphorylated ligand complex; SH2-like domain;
KW   signaling protein; chronic myelogenous leukaemia; CML;
KW   acute lymphocytic leukaemia; ALL; SH2 domain; Lck.
XX
OS   Unidentified.
XX
PN   CA2417838-A1.
XX
PD   01-MAY-1993.
XX
PF   31-OCT-1991;   91CA-02417838.
XX
PR   31-OCT-1991;   91CA-02054602.
```

XX
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
PI Pawson A;
XX
DR WPI; 2003-608536/58.
XX
PT Novel isolated SH2-phosphorylated ligand complex comprising an SH2-like
PT domain or its subdomain and a phosphorylated ligand which is capable of
PT interacting with the SH-2 like domain or its a subdomain.
XX
PS Disclosure; SEQ ID NO 5; 60pp; English.
XX
CC The present invention relates to a SH2-phosphorylated ligand complex
CC comprising an SH2-like domain or its subdomain and a phosphorylated
CC ligand which is capable of interacting with the SH-2 like domain or its a
CC subdomain. The invention also related to a pharmaceutical composition
CC comprising the SH2-phosphorylated ligand complex, which is useful as an
CC agonist or antagonist of the interaction of the signaling protein with a
CC related phosphorylated ligand. The pharmaceutical composition is also
CC useful for treating chronic myelogenous leukaemia (CML), and acute
CC lymphocytic leukaemia (ALL), where the SH2-containing oncoprotein
CC interacts with a signaling protein which is autophosphorylated on serine
CC resulting in transformation. ADN11795-ADN11821 are SH2 domains of
CC signaling proteins, which were used in a sequence alignment.
XX
SQ Sequence 98 AA;

Query Match 100.0%; Score 50; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 82 HYTNASDGL 90

RESULT 9
AAW31184
ID AAW31184 standard; protein; 101 AA.
XX
AC AAW31184;
XX
DT 11-MAR-1998 (first entry)
XX
DE Human p56-lck protein SH2 domain.
XX
KW p62; cytoplasmic; T cell; B cell; development; activation; modulation;
KW cellular response; cell proliferation; autoimmune disease; p56-lck;
KW SH2 binding domain.
XX
OS Homo sapiens.
XX
PN WO9722255-A1.
XX
PD 26-JUN-1997.
XX
PF 11-DEC-1996; 96WO-US019944.
XX
PR 19-DEC-1995; 95US-00574959.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Shin J, Joung I, Vadlamudi RK, Strominger JL;
XX
DR WPI; 1997-341351/31.
XX
PT cDNA encoding p62 and p160 and corresponding proteins - used in the
PT treatment of autoimmune disease and for T and B cell proliferation, e.g.
PT for treatment of tumours.
XX
PS Disclosure; Fig 5; 175pp; English.
XX
CC This sequence represents the p56-lck SH2 binding domain which is capable
CC of binding the p62 sequences represented in AAW31182 and AAW31183 in a
CC phosphotyrosine (pY) independent manner. Such p62 polypeptides with this
CC activity are capable of modulating T or B cell development and/or T or B
CC cell activation e.g. by modulation of Lck activity. They are also capable
CC of modulating degradation of cellular proteins e.g. cell cycle regulatory
CC proteins stimulating expression of cell cycle dependent kinase inhibitors
CC and arresting cell cycle progression at specific boundaries to thereby
CC modulate cell proliferation. As p62 acts to boost B cell response and may
CC be used to treat disorders where this is beneficial, e.g. infections by
CC pathogenic microorganisms, e.g. bacteria, viruses and protozoans. p62 can
CC be used to expand T cell populations for treating infectious diseases or
CC cancer, e.g. the resulting cells may be transduced to render them
CC resistant to HIV infection. Inhibitors of p62 can be used to reduce B or
CC T cell responses and may be used to treat a variety of autoimmune
CC diseases, e.g. diabetes mellitus, arthritis, multiple sclerosis allergic
CC reactions and Crohn's disease
XX
SQ Sequence 101 AA;

Query Match 100.0%; Score 50; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 82 HYTNASDGL 90

RESULT 10
AAR60992
ID AAR60992 standard; peptide; 102 AA.
XX
AC AAR60992;
XX
DT 21-OCT-2004 (revised)
DT 25-MAR-2003 (revised)
DT 14-APR-1995 (first entry)
XX
DE Fragment of p56lck comprising an SH2 region.
XX
KW CD4; T cell; surface antigen; receptor; MHC class II antigen;
KW protein-tyrosine kinase; p56lck; TcR/CD3 complex; PI 3-kinase;
KW PI 4-kinase; lipid kinase; T cell receptor complex; SH2 region.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1. .102
FT /note= "The AA numbering system indicates that there is
FT an AA missing from each line of the SQ"
FT Misc-difference 1
FT /label= W,L
FT Misc-difference 16
FT /label= A,S
FT Misc-difference 31
FT /label= T,Q
FT Misc-difference 61
FT /label= F,V
XX
PN WO9418832-A1.
XX
PD 01-SEP-1994.
XX
PF 25-FEB-1994; 94WO-US001840.
XX
PR 26-FEB-1993; 93US-00023915.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Rudd CE, Kanteti P, Cantley L;
XX
DR WPI; 1994-293868/36.

```
XX
PT   Method for inhibiting or reducing signal transduction - utilises peptide
PT   or corresp. nucleic acid which decreases association of PI 3- or 4-
PT   kinase with CD4/p56lck.
XX
PS   Disclosure; Page 29-30; 46pp; English.
XX
CC   In order for certain T cells to make an optimal response to antigen, it
CC   is necessary for the T cell surface antigen CD4 to couple to the protein-
CC   tyrosine kinase p56lck. (CD4-p56lck is known to associate with and
CC   functionally synergise with the TcR/CD3 complex.)CD4-p56lck complex in T
CC   cells associates with two lipid kinases: PI 3-kinase and PI 4-kinase,
CC   which suggests that these lipid kinases are also involved in
CC   intracellular signalling via the T cell receptor complex. The interaction
CC   of a lipid kinase, such as PI 3-kinase or PI 4- kinase, with CD4-p56lck,
CC   may be blocked by administering a peptide. This peptide may be a fragment
CC   of the cytoplasmic domain of CD4 (eg AAR60987-R60991), a fragment of
CC   p56lck (eg AAR60992, AAR60993), a fragment of PI 3-kinase (eg AAR60994,
CC   AAR60995), or a fragment of PI 4-kinase. Other proline-rich peptides that
CC   bind to SH3 binding sequences can also be used, such as the fragment of
CC   3BP1 protein that binds to the SH3 of the Ab1 kinase (AAR60997), or a
CC   sequence found in the SOS protein (AAR60999). (Updated on 25-MAR-2003 to
CC   correct PN field.)
CC
CC   Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
SQ   Sequence 102 AA;

  Query Match             100.0%;  Score 50;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db         77 HYTNASDGL 85


RESULT 11
AAR72090
ID   AAR72090 standard; protein; 102 AA.
XX
AC   AAR72090;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   27-SEP-1995  (first entry)
XX
DE   Lck SH2 region.
XX
KW   Signal transducer and activator of transcription; STAT; Stat1; Stat91;
KW   receptor recognition factor; transcription factor; cellular debilitation;
KW   derangement; dysfunction; interferon-gamma; SH2 region; Lck.
XX
OS   Unidentified.
XX
PN   WO9508629-A1.
XX
PD   30-MAR-1995.
XX
PF   26-SEP-1994;   94WO-US010849.
XX
PR   24-SEP-1993;   93US-00126588.
PR   24-SEP-1993;   93US-00126595.
PR   11-MAR-1994;   94US-00212184.
PR   11-MAR-1994;   94US-00212185.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Darnell JE,  Schindler CW,  Shuai K,  Wen Z,  Zhong Z;
XX
DR   WPI; 1995-139598/18.
XX
PT   Receptor recognition factor implicated in transcriptional stimulation of
PT   genes - useful in drug screening assays and/or for treating cellular
PT   debilitations, derangements and/or dysfunctions, etc.
XX
PS   Example 6; Page 117; 160pp; English.
XX
CC   A fragment encoding the human Stat91 protein was used to screen a murine
CC   thymus and spleen cDNA for homologous proteins. A highly homologous gene
CC   (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
CC   (Stat1) that was responsive to interferon-gamma. The SH2 region of Stat1
CC   showed homology to SH2 regions of Src, AbI, Lck and p85-alpha-N (AAR72088
CC   -91, respectively). (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 102 AA;

  Query Match             100.0%;  Score 50;  DB 2;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db         83 HYTNASDGL 91


RESULT 12
AAW03982
ID   AAW03982 standard; peptide; 134 AA.
XX
AC   AAW03982;
XX
DT   30-APR-1997  (first entry)
XX
DE   DET1-DET2-spacer-ek-lck SH2 construct.
XX
KW   Polymerase chain reaction; PCR; amplify; primer; chicken; src;
KW   SH2 domain; DET1; DET2; erythropoiesis; anaemia; haematopoiesis;
KW   antagonist.
XX
OS   Synthetic.
XX
PN   EP728482-A2.
XX
PD   28-AUG-1996.
XX
PF   07-FEB-1996;   96EP-00200269.
XX
PR   10-FEB-1995;   95US-00386381.
PR   07-MAR-1995;   95US-00400220.
PR   30-JUN-1995;   95US-00497357.
PR   11-OCT-1995;   95US-00540680.
PR   29-DEC-1995;   95US-00581089.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Dunnington DJ;
XX
DR   WPI; 1996-386024/39.
XX
PT   Use of selective antagonist of haematopoietic acid phosphatase SH2 domain
PT   - with no significant affinity for other SH2 domains, to increase
PT   erythropoiesis and haematopoiesis, esp. for treatment of anaemia.
XX
PS   Example 3; Page 28-29; 46pp; English.
XX
CC   This sequence represents the DET1-DET2-spacer-ek-lck SH2 construct
CC   encoded by the sequence amplified by the primers given in AAT37297-98.
CC   This protein fragment was used in the isolation of a compound for
CC   improving erythropoiesis. The compound may be used for the treatment of
CC   anaemia or to enhance haematopoiesis. The isolated compound antagonises
CC   the hcp SH2 domain without side effects caused by non-specific inhibition
CC   of other SH2 domains
XX
SQ   Sequence 134 AA;
```

```
  Query Match             100.0%;  Score 50;  DB 2;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        112 HYTNASDGL 120


RESULT 13
AAW02120
ID   AAW02120 standard; protein; 134 AA.
XX
AC   AAW02120;
XX
DT   28-OCT-1996  (first entry)
XX
DE   DET1-DET2-spacer-ek-lck SH2 construct.
XX
KW   Bone resorption disease; osteoporosis; src SH2 domain antagonist;
KW   src homology 2 domain; lck SH2 domain.
XX
OS   Homo; sapiens.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          2. .12
FT                   /label= DET1
FT                   /note= "defined epitope tag from HIV-1 gp120/160"
FT   Region          13. .18
FT                   /label= DET2
FT                   /note= "hexahistidine tag"
FT   Region          19. .21
FT                   /label= Spacer
FT   Region          22. .26
FT                   /label= EK
FT                   /note= "enterokinase cleavage site"
FT   Domain          27. .130
FT                   /label= lck-SH2_domain
XX
PN   EP727211-A1.
XX
PD   21-AUG-1996.
XX
PF   07-FEB-1996;   96EP-00200270.
XX
PR   10-FEB-1995;   95US-00386381.
PR   07-MAR-1995;   95US-00400220.
PR   30-JUN-1995;   95US-00497357.
PR   11-OCT-1995;   95US-00541080.
PR   29-DEC-1995;   95US-00580868.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Dunnington DJ;
XX
DR   WPI; 1996-372674/38.
XX
PT   Use of selective src SH2 domain ligand - to prepare medicament for
PT   treating bone resorption disease.
XX
PS   Example 11; Page 28-29; 47pp; English.
XX
CC   Construct DET1-DET2-spacer-ek-lck SH2 (AAW02120) was obtd. by inserting a
CC   PCR fragment (see also AAT36190-91) coding for human lck SH2 domain into
CC   a vector contg. a tagged chicken src gene DET1-DET2-spacer-SH2 (see also
CC   AAT36186-87). The construct can be expressed in E. coli and used,
CC   together with similar constructs (see also AAW02119-21 and AAW02124-27),
CC   in binding assays to determine the specificity of cpds. to inhibit SH2
CC   domains; cpds. that selectively inhibit the human src SH2 domain are
CC   useful in treating bone resorption diseases such as osteoporosis
XX
SQ   Sequence 134 AA;

  Query Match             100.0%;  Score 50;  DB 2;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        112 HYTNASDGL 120


RESULT 14
AAW11286
ID   AAW11286 standard; peptide; 134 AA.
XX
AC   AAW11286;
XX
DT   10-NOV-1997  (first entry)
XX
DE   DET1-DET2-spacer-ek-lck SH2 fusion protein.
XX
KW   HIV-1; gp120; defined epitope tag; DET1; envelope protein; human; Stat 6;
KW   signal transduction and activation of transcription; Src homology 2;
KW   signalling molecule; protein tyrosine kinase; oncogenic protein; hcp SH2;
KW   Grb2 SH2; allergic reaction; erythrocyte production; inhibitor; p85 SH2;
KW   asthma; allergic rhinitis; atopic dermatitis; IgE receptor; SH-PTP2 SH2;
KW   interleukin-4; IL-4; SH2 domain; Stat5 SH2; src SH2; lck SH2; fyn SH2;
KW   IL-13; therapy; fusion protein.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         2. .12
FT                   /note= "defined epitope tag 1 (DET1)"
FT   Peptide         13. .18
FT                   /note= "defined epitope tag 2 (DET2)"
FT   Peptide         19. .21
FT                   /note= "spacer"
FT   Peptide         22. .26
FT                   /note= "enteroprotein kinase recognition sequence"
FT   Peptide         27. .134
FT                   /note= "human lck SH2 domain"
XX
PN   WO9702023-A1.
XX
PD   23-JAN-1997.
XX
PF   28-JUN-1996;   96WO-US011074.
XX
PR   30-JUN-1995;   95US-00497357.
PR   08-FEB-1996;   96US-00598716.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Dunnington DJ;
XX
DR   WPI; 1997-108735/10.
XX
PT   Treating allergies with specific inhibitor of human Stat 6 SH2 domain -
PT   having very low binding affinity to panel of other SH2 domains so free of
PT   side effects, specifically for asthma and allergic rhinitis.
XX
PS   Example 11; Page 51-52; 88pp; English.
XX
CC   AAW11285-W11288 represent fusion proteins containing Src homology 2 (SH2)
CC   domains. These sequences are used to identify a compound that targets the
CC   human Stat (signal transduction and activation of transcription) 6 SH2
CC   domain. The identified compounds have a binding affinity for Stat 6 over
CC   50 (preferably 100) times higher than its affinity for the human Stat5
CC   SH2 domain. The compound has an affinity for hcp SH2, SH-PTP2 SH2, p85
CC   SH2, Grb2 SH2, src SH2, lck SH2 or fyn SH2 of more than 50 (preferably
CC   100) times lower than its affinity for Stat 6 SH2. SH2 domains are
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CC   conserved non-catalytic sequences found in a variety of signalling
CC   molecules, such as non-receptor protein tyrosine kinases, and in
CC   oncogenic proteins. The compounds identified using the fusion proteins
CC   are used as the administered compound in the method of the invention for
CC   treating allergic reactions. Administration of the compound avoids the
CC   side effects (e.g. reduced erythrocyte production) associated with non-
CC   selective inhibition of SH2 domains. Selective compounds can be
CC   identified in competitive binding assays using only a small subset (the
CC   domains specified above) of SH2 domains rather than all 60 known domains.
CC   The method can be used for the treatment of asthma and allergic rhinitis,
CC   but can also be used to treat atopic dermatitis. Inhibition of the human
CC   Stat 6 SH2 domain blocks up-regulation of the IgE receptor mediated by
CC   interleukin-4 (IL-4) or IL-13
XX
SQ   Sequence 134 AA;

  Query Match             100.0%;  Score 50;  DB 2;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        112 HYTNASDGL 120


RESULT 15
AAW19624
ID   AAW19624 standard; protein; 134 AA.
XX
AC   AAW19624;
XX
DT   27-OCT-1997  (first entry)
XX
DE   Human lck SH2 domain fusion protein.
XX
KW   Stat 5; Signal Transduction and Activation of Transcription;
KW   Src homology domain; SH2; erythropoiesis enhancing; anaemia;
KW   fusion protein; ek; enterokinase; epitope; antibody production;
KW   detection; HIV; human immunodeficiency virus type 1; gp120;
KW   glycoprotein 120; selective.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         2. .12
FT                   /note= "defined epitope tag 1 from HIV gp120"
FT   Peptide         13. .18
FT                   /note= "hexahistidine sequence tag"
FT   Region          19. .21
FT                   /label= spacer
FT   Cleavage-site   22. .26
FT                   /note= "enterokinase protease recognition site"
FT   Peptide         27. .134
FT                   /note= "lck SH2"
XX
PN   WO9702024-A1.
XX
PD   23-JAN-1997.
XX
PF   28-JUN-1996;   96WO-US011158.
XX
PR   30-JUN-1995;   95US-00497357.
PR   08-FEB-1996;   96US-00598715.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Dunnington DJ;
XX
DR   WPI; 1997-108736/10.
XX
PT   Enhancing erythropoiesis with specific activator of human Stat 5 SH2
PT   domain - has very low binding affinity to other SH2 domains so free of
PT   side effects, particularly for treating anaemia.
XX
PS   Example 11; Page 54-55; 91pp; English.
XX
CC   AAW19624 is a fusion protein of formula DET1-DET2-Sp-ek-SH2, where DET1
CC   is a defined epitope tag from HIV-1 gp120, DET2 is a hexahistidine
CC   sequence tag (binds to nickel-containing resins, used for purification),
CC   Sp is a spacer, ek is an enterokinase protease recognition site and SH2
CC   is the human lck SH2 domain. DET1 is included so that antibodies against
CC   the epitope can be used to detect the recombinant expression of the
CC   fusion protein and hence the SH2 domain. The fusion proteins are used for
CC   identifying compounds that bind the SH2 domain causing its activation
XX
SQ   Sequence 134 AA;

  Query Match             100.0%;  Score 50;  DB 2;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        112 HYTNASDGL 120


RESULT 16
AAW14788
ID   AAW14788 standard; protein; 224 AA.
XX
AC   AAW14788;
XX
DT   20-JUN-1997  (first entry)
XX
DE   FKBP-LCK:SH2 fusion protein.
XX
KW   FKBP-LCK:SH2; FK506 binding protein; SH2 domain; Src homology 2;
KW   fusion protein; high throughput assay; signal transduction; ligand;
KW   microscintillation.
XX
OS   Homo sapiens.
XX
PN   WO9710253-A1.
XX
PD   20-MAR-1997.
XX
PF   11-SEP-1996;   96WO-US014567.
XX
PR   15-SEP-1995;   95US-0003819P.
PR   12-MAR-1996;   96GB-00005210.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Marcy A,  Salowe SP,  Wisniewski D;
XX
DR   WPI; 1997-202171/18.
DR   N-PSDB; AAT63421.
XX
PT   Screening compounds for binding to fusion proteins with defined ligands -
PT   allows high capacity assays and identification of (ant)agonists or
PT   inhibitors for drug development.
XX
PS   Claim 32; Page 21-22; 36pp; English.
XX
CC   Novel fusion proteins FKBP-ZAP:SH2, FKBP-SYK:SH2 and FKBP-LCK:SH2
CC   (AAW14786-88) comprise FK506 binding protein (FKBP) linked via a peptide
CC   linker to a target protein composed of a multiple signal transduction
CC   domain, i.e. ZAP:SH2, SYK:SH2 or LCK:SH2. They can be produced in
CC   transformed host cells, esp. E. coli, using expression vectors with
CC   fusion protein DNA sequences (AAT63419-21). The fusion proteins are used
CC   in novel methods utilising microscintillation plate technology for the
CC   functional assay of ligand binding to a signal transduction domain (i.e.
CC   SH2). The method is readily adaptable to robotic automation for high
CC   capacity screening for agonists, antagonists and/or inhibitors for use in
CC   drug development
XX
```

SQ Sequence 224 AA;

Query Match 100.0%; Score 50; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 206 HYTNASDGL 214

RESULT 17
AAW96823
ID AAW96823 standard; protein; 224 AA.
XX
AC AAW96823;
XX
DT 21-APR-1999 (first entry)
XX
DE A fusion protein of FKBP-Lck.
XX
KW Fusion protein; FK506 binding protein; FKBP; SH2 domain; human Lck;
KW screening; protein binding; ligand-protein interaction;
KW protein-protein interaction; protease inhibitor.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9841866-A1.
XX
PD 24-SEP-1998.
XX
PF 10-MAR-1998; 98WO-US004610.
XX
PR 14-MAR-1997; 97US-0040795P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Hermes JD, Salowe SP, Sinclair PJ;
XX
DR WPI; 1999-070061/06.
DR N-PSDB; AAX15151.
XX
PT High throughput screening assay - for screening compounds capable of
PT binding to a fusion protein consisting of, e.g., a target protein and an
PT FK506-binding protein.
XX
PS Disclosure; Page 26; 42pp; English.
XX
CC The present sequence represents a fusion protein comprising FK506 binding
CC protein (FKBP) and the SH2 domain of human Lck. The protein is used to
CC exemplify the method of the invention. The specification describes a
CC method for screening for compounds capable of binding to a fusion
CC protein. The method comprises mixing a test compound, a biotinylated
CC ligand, the fusion protein, a donor-labelled ligand and acceptor-labeled
CC streptavidin, incubating the mixture, measuring the time-resolved
CC fluorescence attributable to the binding of the biotinylated ligand to
CC the fusion protein in the presence of the test compound and determining
CC the binding of the biotinylated ligand to the fusion protein in the
CC presence of the test compound relative to a control assay run in the
CC absence of the test compound. The methods may be used to determine if
CC compounds are capable of binding to a protein or are capable of blocking
CC ligand-protein or protein-protein interactions. They may be used to
CC identify compounds which are protease inhibitors
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 50; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 206 HYTNASDGL 214

RESULT 18
ABR59690
ID ABR59690 standard; protein; 363 AA.
XX
AC ABR59690;
XX
DT 25-JUL-2003 (first entry)
XX
DE Human p56lck.
XX
KW Human; T lymphocyte activation; T-cell; A-raf-1; TCPTP/PTPN2; asthma;
KW immunosuppressive; antiasthmatic; antiallergic; antiinflammatory;
KW lymphocyte activation; lymphocyte migration; cytokine production;
KW cell surface marker expression; antibody production; apoptosis; allergy;
KW antibody proliferation; antibody differentiation; hypersensitivity;
KW graft versus host disease; inflammation; p56lck.
XX
OS Homo sapiens.
XX
PN WO2003029277-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031618.
XX
PR 03-OCT-2001; 2001US-0327212P.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Chu P, Li C, Liao XC, Masuda E, Pardo J, Zhao H;
XX
DR WPI; 2003-363276/34.
DR N-PSDB; ACC81082.
XX
PT Identifying a compound that modulates T lymphocyte activation, useful for
PT monitoring changes in cell surface marker expression, comprises
PT contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with
PT a compound.
XX
PS Disclosure; Page 64; 126pp; English.
XX
CC The invention relates to a novel method for identifying a compound that
CC modulates T lymphocyte activation. The method comprises contacting a T
CC cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound,
CC where the A-raf- 1 or TCPTP/PTPN2 polypeptide is encoded by a nucleic
CC acid that hybridises to a nucleic acid encoding a polypeptide having a
CC sequence selected from two 606-amino acid sequence and a 415-amino acid
CC sequence given in the specification. The method of the invention has
CC immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory
CC activity. The method is useful for identifying compounds that modulate
CC lymphocyte activation and migration, and for monitoring changes in cell
CC surface marker expression, cytokine production, antibody production,
CC proliferation and differentiation, and apoptosis, using either cell lines
CC or primary cells. The A-raf- 1 or TCPTP/PTPN2 proteins may be used as
CC drug targets for compounds that suppress or activate lymphocyte
CC activation and migration, e.g. for the treatment of diseases in which
CC modulation of the immune response is desired such as delayed type
CC hypersensitivity reactions, asthma, allergies, graft versus host disease,
CC and acute and chronic inflammation. Modulators of lymphocyte activation
CC are useful for treating disorders related T and B cell activation and
CC migration. The present sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 363 AA;

Query Match 100.0%; Score 50; DB 6; Length 363;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9

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              |||||||||
Db        208 HYTNASDGL 216


RESULT 19
ADP48375
ID   ADP48375 standard; protein; 363 AA.
XX
AC   ADP48375;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human lymphocyte specific tyrosine kinase (Lck) polypeptide #2.
XX
KW   Human; lymphocyte specific tyrosine kinase; Lck;
KW   antisense oligonucleotide; phosphorothioate linkage;
KW   2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
KW   hyperproliferative disorder; cancer; cytostatic; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2004116365-A1.
XX
PD   17-JUN-2004.
XX
PF   10-DEC-2002; 2002US-00316515.
XX
PR   10-DEC-2002; 2002US-00316515.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Borchers AH,  Freier SM;
XX
DR   WPI; 2004-498280/47.
DR   N-PSDB; ADP48372.
XX
PT   New antisense oligonucleotide compounds, useful for diagnosing,
PT   preventing and/or treating diseases or conditions associated with
PT   aberrant expression or activity of Lck, such as hyperproliferative
PT   disorders.
XX
PS   Example 17; SEQ ID NO 75; 40pp; English.
XX
CC   The invention relates to a compound targeted to a nucleic acid molecule
CC   encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.
CC   The compound is an antisense oligonucleotide that specifically hybridises
CC   with the nucleic acid and inhibits expression of the polypeptide. The
CC   antisense oligonucleotide comprises at least one modified internucleoside
CC   linkage i.e. a phosphorothioate linkage, at least one modified sugar
CC   moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one
CC   modified nucleobase comprising a 5-methylcytosine. The antisense
CC   compounds are useful for modulating the expression of the human Lck
CC   polypeptide and in preparation of a composition for treating
CC   hyperproliferative disorders, e.g. cancer. This sequence represents a
CC   human Lck polypeptide of the invention.
XX
SQ   Sequence 363 AA;

  Query Match             100.0%;  Score 50;  DB 8;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        208 HYTNASDGL 216


RESULT 20
ABG79672
ID   ABG79672 standard; protein; 437 AA.
XX
AC   ABG79672;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Tumour involved gene (TIG) splice variant protein, NV-3.
XX
KW   Human; splice variant; tumour-involved gene; TIG;
KW   pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
KW   endothelial cell; cell differentiation; cell proliferation; apoptosis;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2002086384-A1.
XX
PD   04-JUL-2002.
XX
PF   13-MAR-2001; 2001US-00805020.
XX
PR   14-MAR-2000; 2000IL-00135402.
PR   16-MAY-2000; 2000IL-00136154.
XX
PA   (LEVI/) LEVINE Z.
PA   (DAVI/) DAVID A.
PA   (ROMA/) ROMANO C.
PA   (BERN/) BERNSTEIN J.
XX
PI   Levine Z,  David A,  Romano C,  Bernstein J;
XX
DR   WPI; 2002-635679/68.
DR   N-PSDB; ABS65202.
XX
PT   Novel nucleic acid sequence, which is an alternative splicing variant of
PT   tumor involved genes, useful for detecting cancer, predisposition to
PT   cancer, for evaluating cancer state and in gene therapy for treating
PT   cancer.
XX
PS   Claim 4; Page 68-69; 180pp; English.
XX
CC   The invention discloses isolated human nucleic acid alternative splicing
CC   variants that are all tumour-involved genes (TIGs). The nucleic acids and
CC   polypeptides are useful for determining the level of a nucleic acid or
CC   polypeptide in a biological sample, for detecting a variant nucleic acid
CC   or polypeptide sequence in a biological sample, for determining the level
CC   of variant nucleic acid or polypeptide sequences in a biological sample
CC   and for determining the ratio between the level of variant sequence in a
CC   first biological sample and the level of the original sequence from which
CC   the variant has been varied by alternative splicing in a second
CC   biological sample and for raising antibodies. A pharmaceutical
CC   composition comprising a carrier and the nucleic acid, is useful for
CC   treating diseases (e.g. cancer) that can be ameliorated or cured by
CC   increasing or decreasing the level of the encoded protein. The nucleic
CC   acids are also useful for diagnostic purposes, especially for detecting
CC   cancer or a predisposition to cancer, for evaluating the state or
CC   aggressiveness of cancer disease, in basic research, for understanding
CC   the physiological function of the original TIG, in targeting or
CC   developing pharmaceuticals, for distinguishing various stages in the life
CC   cycle of the same type of cells which may be helpful for the development
CC   of pharmaceuticals for various cancer stages in which cell cycle is non-
CC   normal, for determining mutations in tumour-involved genes and in gene
CC   therapy. The polypeptides are useful for identifying compounds capable of
CC   binding to the variant product and modulating its activity and for
CC   modulating endothelial differentiation and proliferation, as well as to
CC   modulate apoptosis either ex vivo or in vivo. The sequences presented in
CC   ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
CC   disclosed
XX
SQ   Sequence 437 AA;

  Query Match             100.0%;  Score 50;  DB 5;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
```

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Db        208 HYTNASDGL 216


RESULT 21
AAB37700
ID   AAB37700 standard; protein; 508 AA.
XX
AC   AAB37700;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human lymphocyte kinase.
XX
KW   Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
XX
OS   Homo sapiens.
XX
PN   WO200070030-A1.
XX
PD   23-NOV-2000.
XX
PF   19-MAY-2000; 2000WO-US013881.
XX
PR   19-MAY-1999;   99US-0134965P.
XX
PA   (KINE-) KINETIX PHARM INC.
XX
PI   Zhu X;
XX
DR   WPI; 2000-687708/67.
XX
PT   Crystal of a protein-ligand complex for identifying kinase inhibitors,
PT   comprises a truncated lymphocyte kinase and a ligand, and diffracts X-
PT   rays to determine atomic coordinates at a resolution greater than 5
PT   angstroms.
XX
PS   Claim 1; Page 434-5; 438pp; English.
XX
CC   The present invention relates to a crystal of a protein-ligand complex
CC   comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal
CC   diffracts X-rays so that the atomic coordinates of the protein-ligand
CC   complex can be determined to a resolution of greater than 5.0 Angstroms.
CC   The truncated lck used in the present invention comprises the globular
CC   core of the corresponding full-length lck. The present sequence is the
CC   full-length human lck protein. The crystal of the present invention may
CC   be used to identify kinase inhibitors in screening assays, in drug
CC   screening and drug design processes, to design, select or test inhibitors
CC   of kinase enzymes, where the inhibitors are used as therapeutics for the
CC   treatment and modulation of diseases, disease symptoms or the effect of
CC   other physiological events mediated by kinases, having one or more kinase
CC   enzymes involved in their pathology
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 50;  DB 3;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        207 HYTNASDGL 215


RESULT 22
ADE58802
ID   ADE58802 standard; protein; 508 AA.
XX
AC   ADE58802;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06239, SEQ ID NO 4689.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 50;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        207 HYTNASDGL 215


RESULT 23
ADE58799
ID   ADE58799 standard; protein; 508 AA.
XX
AC   ADE58799;
```

XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P06239, SEQ ID NO 4686.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P06239.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 50; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 207 HYTNASDGL 215

RESULT 24
ADF45072
ID ADF45072 standard; protein; 508 AA.
XX
AC ADF45072;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human kinase LCK.
XX
KW Human; protein kinase; enzyme; inhibitor; LCK.
XX
OS Homo sapiens.
XX
PN WO2003081210-A2.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-US008725.
XX
PR 21-MAR-2002; 2002US-0366892P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Prescott JC, Braisted A;
XX
DR WPI; 2003-865136/80.
XX
PT Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.
XX
PS Disclosure; SEQ ID NO 41; 260pp; English.
XX
CC The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 50; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 207 HYTNASDGL 215

RESULT 25
ADL34479
ID ADL34479 standard; peptide; 508 AA.
XX
AC ADL34479;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human lymphocyte kinase (Lck) globular core.
XX
KW cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;
KW fungicide; nootropic; neuroprotective; kinase inhibitor; crystal;
KW protein-ligand complex; lymphocyte kinase; Lck; Lck ligand;
KW kinase inhibitor; therapeutic; kinase-mediated physiological event;
KW cancer; autoimmunological; metabolic; inflammatory; infection;
KW central nervous system degenerative disease; transplant rejection; human;

KW globular core; protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN US6589758-B1.
XX
PD 08-JUL-2003.
XX
PF 21-MAY-2001; 2001US-00862154.
XX
PR 19-MAY-2000; 2000US-0205510P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zhu X;
XX
DR WPI; 2003-810380/76.
XX
PT Crystal of protein-ligand complex useful for identifying an inhibitor of
PT lymphocyte kinase (Lck), comprises truncated Lck and a ligand.
XX
PS Claim 1; SEQ ID NO 1; 295pp; English.
XX
CC The invention describes a crystal (I) of a protein-ligand complex (C)
CC comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I)
CC effectively diffracts X-rays for determination of atomic coordinates of
CC (C) to a resolution of greater than 5.0 angstroms, and truncated Lck
CC comprises a sequence (S1) of residues 225-508 of a 508 amino acid
CC sequence, given in specification and retains the globular core of full-
CC length Lck. (I) is useful in an inhibitor screening assay and to
CC identify, design, select, and evaluate potential inhibitors of kinases
CC that would be useful as therapeutics for diseases or symptoms of diseases
CC that are associated with kinase-mediated physiological events. The
CC inhibitors identified by the methods may also be useful for inhibition of
CC kinase activity of one or more enzymes. The inhibitors are also useful
CC for inhibiting the biological activity of any enzyme comprising greater
CC than 90%, alternatively greater than 85%, or alternatively greater than
CC 70% sequence homology with a kinase sequence. The inhibitors are useful
CC for inhibiting the biological activity of any enzyme that binds ATP and
CC thus for treating disease or disease symptoms mediated by any enzyme that
CC binds ATP. The inhibitors are useful in inhibiting kinase activity and
CC are useful in treating kinase-mediated disease or disease symptoms in a
CC mammal, particularly a human e.g., cancer, autoimmunological, metabolic,
CC inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central
CC nervous system degenerative disease etc. The inhibitors are useful in
CC treating or preventing diseases, including, transplant rejection etc.
CC This is the amino acid sequence of a human lymphocyte kinase (Lck)
CC polypeptide comprising the Lck globular core.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 50; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 207 HYTNASDGL 215

RESULT 26
ADS88148
ID ADS88148 standard; protein; 508 AA.
XX
AC ADS88148;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
XX
KW protein complex; tumour necrosis factor-alpha signalling pathway;
KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004035783-A2.
XX
PD 29-APR-2004.
XX
PF 24-SEP-2003; 2003WO-EP050655.
XX
PR 26-SEP-2002; 2002EP-00021809.
PR 10-FEB-2003; 2003EP-00100274.
XX
PA (CELL-) CELLZOME AG.
XX
PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI Superti-Furga G, Kruse U;
XX
DR WPI; 2004-348460/32.
XX
PT New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.
XX
PS Example; SEQ ID NO 3; 1980pp; English.
XX
CC This invention relates to novel protein complexes of the tumour necrosis
CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 50; DB 8; Length 508;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 207 HYTNASDGL 215

RESULT 27
AAY49420
ID AAY49420 standard; protein; 509 AA.
XX
AC AAY49420;
XX
DT 13-MAR-2000 (first entry)
XX
DE PKA substrate, Src-family protein.
XX
KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW kinase substrate; immunosuppressive disorder; proliferative disease;
KW HIV infection; AIDS; immunodeficiency; autoimmune disease;

KW systemic lupus erythematosus; Src-family.
XX
OS Homo sapiens.
XX
PN WO9962315-A2.
XX
PD 02-DEC-1999.
XX
PF 27-MAY-1999; 99WO-GB001680.
XX
PR 27-MAY-1998; 98NO-00002419.
PR 30-DEC-1998; 98US-0114240P.
XX
PA (LAUR-) LAURAS AS.
PA (JONE/) JONES E L.
XX
PI Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V;
PI Tasken K, Vang T, Altman A, Munshi A;
XX
DR WPI; 2000-086801/07.
DR N-PSDB; AAZ46491.
XX
PT Altering the activity of protein kinase signaling pathways, used for
PT treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,
PT e.g. cancers or autoimmune diseases.
XX
PS Claim 23; Page 95-96; 111pp; English.
XX
CC The invention provides a novel method of altering the activity of the
CC protein kinase A (PKA) signaling pathway in a cell that comprises
CC altering the extent of phosphorylation of one or more PKA substrates, or
CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC compositions containing a nucleic acid molecule that encodes a PKA
CC substrate, or fragment, precursor or functionally equivalent variant,
CC where the sequence is modified to alter its susceptibility to
CC phosphorylation by PKA can be used for treating a disorder exhibiting
CC abnormal PKA signaling activity, immunosuppressive disorders or
CC proliferative diseases. They can be used for treating e.g. HIV infection,
CC AIDS, common variable immunodeficiency or cancers. Conditions in which
CC upregulation of the PKA pathway is required, such as autoimmune disease,
CC e.g. systemic lupus erythematosus, may also be treated. The present
CC sequence represents a PKA substrate, wherein the substrate is in the Src-
CC family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl,
CC Fyk, Src-1 or Src-2
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 50; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 208 HYTNASDGL 216

RESULT 28
ABR58699
ID ABR58699 standard; protein; 509 AA.
XX
AC ABR58699;
XX
DT 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:356.
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO2003025138-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029560.
XX
PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
DR WPI; 2003-354600/33.
DR N-PSDB; ACC72850.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 762; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 50; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 208 HYTNASDGL 216

RESULT 29
ABR56202
ID ABR56202 standard; protein; 509 AA.
XX
AC ABR56202;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Lymphocyte Cell Kinase, Lck.
XX
KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW Src-family protein tyrosine kinase; T-cell; immune response.
XX
OS Homo sapiens.
XX
PN WO2003020880-A2.

XX
PD 13-MAR-2003.
XX
PF 02-AUG-2002; 2002WO-US024546.
XX
PR 03-AUG-2001; 2001US-0310051P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;
PI Leung A, Ritter K;
XX
DR WPI; 2003-300872/29.
XX
PT New crystalline polypeptide comprising ligand binding domain or catalytic
PT domain of Lck protein, for determining three-dimensional structure of
PT catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS Claim 5; Fig 1; 994pp; English.
XX
CC The present invention relates to a crystalline polypeptide (I),
CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC in T-cells and plays an essential role in immune response. The present
CC sequence is the full-length sequence of human Lck (1-509). (I) is useful
CC for identifying a compound which is an inhibitor of human Lck protein
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 50; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 208 HYTNASDGL 216

RESULT 30
ADE40449
ID ADE40449 standard; protein; 509 AA.
XX
AC ADE40449;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human proto-oncogene Tyr protein kinase LCK (gene ID 1611) protein.
XX
KW AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;
KW HIV-related disorder; differential expression; drug screening;
KW viral replication modulation; diagnosis; prognosis; predisposition;
KW anti-HIV; gene therapy; antisense therapy; human;
KW proto-oncogene Tyr protein kinase LCK; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003070883-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004246.
XX
PR 15-FEB-2002; 2002US-0357391P.
PR 13-MAY-2002; 2002US-0380249P.
PR 25-JUN-2002; 2002US-0391306P.
PR 27-AUG-2002; 2002US-0406297P.
PR 19-SEP-2002; 2002US-0412007P.
PR 10-OCT-2002; 2002US-0417508P.
PR 10-DEC-2002; 2002US-0432318P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Powell DM, Weich NS;
XX
DR WPI; 2003-671808/63.
DR N-PSDB; ADE40448.
XX
PT Identifying a compound capable of diagnosing, preventing or treating AIDS
PT or an HIV-related disorder comprises assaying the ability of the compound
PT to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or
PT polypeptide activity.
XX
PS Claim 1; SEQ ID NO 28; 167pp; English.
XX
CC The invention relates to a method of identifying a compound useful in the
CC treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human
CC immunodeficiency virus)-related disorder. The invention involves assaying
CC the ability of a test compound to modulate the activity or expression of
CC 26 human proteins. These proteins and nucleic acids encoding them
CC (ADE40422-ADE40473) are differentially expressed in tissues relating to
CC AIDS or an HIV-related disorder compared to their expression in normal
CC tissues. The invention also relates to the use of the compounds
CC identified to modulate viral replication in a cell and to treat a patient
CC with AIDS or an HIV-related disorder. The invention further discloses
CC methods for the diagnostic evaluation and prognosis of various HIV-
CC related disorders, and for the identification of individuals exhibiting a
CC predisposition to such conditions. The modulatory compounds identified
CC using the method of the invention may be small organic molecules,
CC peptides, antibodies or antisense nucleic acid molecules. The methods of
CC the invention are useful in diagnosing, preventing or treating AIDS or
CC HIV-related disorders. The present sequence represents a human protein
CC which is differentially expressed in AIDS or HIV-related disorders.
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 50; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9
|||||||||
Db 208 HYTNASDGL 216

Search completed: June 29, 2006, 09:13:15
Job time : 90.8313 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 105.831 Seconds
(without alignments)
78.664 Million cell updates/sec

Title: US-10-062-257A-3
Perfect score: 50
Sequence: 1 HYTNASDGL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	368	2	Q3TLX4_MOUSE	Q3tlx4 mus musculu
2	50	100.0	379	2	Q4FZR6_RAT	Q4fzr6 rattus norv
3	50	100.0	508	1	LCK_AOTNA	Q5pxs1 aotus nancy
4	50	100.0	508	1	LCK_HUMAN	P06239 homo sapien
5	50	100.0	508	1	LCK_MOUSE	P06240 mus musculu
6	50	100.0	508	1	LCK_SAISC	Q95kr7 saimiri sci
7	50	100.0	509	2	Q7RTZ3_HUMAN	Q7rtz3 homo sapien
8	50	100.0	509	2	Q95M32_9PRIM	Q95m32 hylobates s
9	41	82.0	450	2	O73786_XENLA	O73786 xenopus lae
10	40	80.0	193	2	Q81295_9HEPC	Q81295 hepatitis c
11	40	80.0	408	2	Q4R6L8_MACFA	Q4r6l8 macaca fasc
12	40	80.0	505	1	FRK_HUMAN	P42685 homo sapien
13	40	80.0	505	2	Q9NTR5_HUMAN	Q9ntr5 homo sapien
14	40	80.0	509	2	Q3ZCM0_BOVIN	Q3zcm0 bos taurus
15	39	78.0	323	2	Q9SH39_ARATH	Q9sh39 arabidopsis
16	39	78.0	324	2	Q5Q0E2_ARATH	Q5q0e2 arabidopsis
17	38	76.0	276	2	Q38KH2_BOVIN	Q38kh2 bos taurus
18	38	76.0	525	2	Q8AWF1_BRARE	Q8awf1 brachydanio
19	38	76.0	943	2	Q7QE10_ANOGA	Q7qe10 anopheles g
20	38	76.0	1114	2	Q2PBR5_9VIRU	Q2pbr5 tellina vir
21	37	74.0	351	2	Q6IJB6_DROME	Q6ijb6 drosophila
22	37	74.0	358	2	Q6W9M4_PENMA	Q6w9m4 penicillium
23	37	74.0	359	2	Q5DPY8_PARBR	Q5dpy8 paracoccidi
24	37	74.0	359	2	Q2URQ7_ASPOR	Q2urq7 aspergillus
25	37	74.0	359	2	Q4WYB0_ASPFU	Q4wyb0 aspergillus
26	37	74.0	360	2	Q60Q64_CAEBR	Q60q64 caenorhabdi
27	37	74.0	361	2	Q9Y7E3_EMENI	Q9y7e3 emericella
28	37	74.0	361	2	Q5B8P0_EMENI	Q5b8p0 aspergillus
29	37	74.0	368	2	Q4VT41_CAEBR	Q4vt41 caenorhabdi
30	37	74.0	405	2	Q4URA6_XANC8	Q4ura6 xanthomonas
31	37	74.0	405	2	Q8PC78_XANCP	Q8pc78 xanthomonas
32	37	74.0	440	2	Q31981_CYSFR	Q31981 cystopteris
33	37	74.0	520	2	Q73YI8_MYCPA	Q73yi8 mycobacteri
34	37	74.0	535	2	Q9CBT1_MYCLE	Q9cbt1 mycobacteri
35	37	74.0	558	2	Q8L299_PROVU	Q8l299 proteus vul
36	37	74.0	563	2	Q6R1Y3_ASTMI	Q6r1y3 asterina mi
37	37	74.0	696	2	Q47RD2_THEFY	Q47rd2 thermobifid
38	37	74.0	825	2	Q8A2K5_BACTN	Q8a2k5 bacteroides
39	37	74.0	973	2	Q4P1B5_USTMA	Q4p1b5 ustilago ma
40	36	72.0	160	2	Q31X08_SHIBS	Q31x08 shigella bo
41	36	72.0	271	2	Q3ZB94_BRARE	Q3zb94 brachydanio
42	36	72.0	301	2	Q6FM74_CANGA	Q6fm74 candida gla
43	36	72.0	311	2	Q6CL53_KLULA	Q6cl53 kluyveromyc
44	36	72.0	320	2	Q41NX2_METBU	Q41nx2 methanococc
45	36	72.0	345	1	GCH2_YEAST	P38066 saccharomyc
46	36	72.0	436	2	Q9KVG7_VIBCH	Q9kvg7 vibrio chol
47	36	72.0	440	2	Q54US8_DICDI	Q54us8 dictyosteli
48	36	72.0	449	2	Q53EL3_HUMAN	Q53el3 homo sapien
49	36	72.0	450	1	CSK_HUMAN	P41240 homo sapien
50	36	72.0	450	2	Q2M3N2_HUMAN	Q2m3n2 homo sapien
51	36	72.0	462	2	Q2W5L4_MAGSA	Q2w5l4 magnetospir
52	36	72.0	505	2	Q9VYH4_DROME	Q9vyh4 drosophila
53	36	72.0	514	2	Q4E5Q5_TRYCR	Q4e5q5 trypanosoma
54	36	72.0	587	2	Q2UV32_ASPOR	Q2uv32 aspergillus
55	36	72.0	616	2	Q6S890_MANSM	Q6s890 mannheimia
56	36	72.0	616	2	Q9CP37_PASMU	Q9cp37 pasteurella
57	36	72.0	635	2	Q6K3D8_ORYSA	Q6k3d8 oryza sativ
58	36	72.0	644	2	Q72NC9_LEPIC	Q72nc9 leptospira
59	36	72.0	644	2	Q8F862_LEPIN	Q8f862 leptospira
60	36	72.0	730	2	Q6D183_ERWCT	Q6d183 erwinia car
61	36	72.0	890	2	Q75AI4_ASHGO	Q75ai4 ashbya goss
62	36	72.0	1056	2	Q386H8_9TRYP	Q386h8 trypanosoma
63	35	70.0	47	2	Q68VG9_9BASI	Q68vg9 uncultured
64	35	70.0	47	2	Q70U76_9HOMO	Q70u76 xerocomus c
65	35	70.0	47	2	Q70UH8_9BASI	Q70uh8 uncultured
66	35	70.0	47	2	Q2PCX0_9BASI	Q2pcx0 uncultured
67	35	70.0	47	2	Q2PCX2_9BASI	Q2pcx2 uncultured
68	35	70.0	47	2	Q2PD09_9BASI	Q2pd09 uncultured
69	35	70.0	47	2	Q2PD22_9BASI	Q2pd22 uncultured
70	35	70.0	120	2	Q98TP5_PLAFE	Q98tp5 platichthys
71	35	70.0	160	1	YGIV_ECO57	Q8xbs4 escherichia
72	35	70.0	160	1	YGIV_ECOLI	Q46866 escherichia
73	35	70.0	160	2	Q32BT0_SHIDS	Q32bt0 shigella dy
74	35	70.0	160	2	Q3YXL6_SHISS	Q3yxl6 shigella so
75	35	70.0	160	2	Q2M9H7_ECOLI	Q2m9h7 escherichia
76	35	70.0	160	2	Q83JL0_SHIFL	Q83jl0 shigella fl
77	35	70.0	266	2	Q40IG5_EHRCH	Q40ig5 ehrlichia c
78	35	70.0	273	2	Q427K3_DESHA	Q427k3 desulfitoba
79	35	70.0	302	2	Q40HT4_9RHOB	Q40ht4 jannaschia
80	35	70.0	330	2	Q3EJK6_BACTI	Q3ejk6 bacillus th
81	35	70.0	341	2	Q4MS64_BACCE	Q4ms64 bacillus ce
82	35	70.0	341	2	Q633Y5_BACCZ	Q633y5 bacillus ce
83	35	70.0	341	2	Q81LD2_BACAN	Q81ld2 bacillus an
84	35	70.0	341	2	Q72ZW7_BACC1	Q72zw7 bacillus ce
85	35	70.0	364	2	Q396G8_BURS3	Q396g8 burkholderi
86	35	70.0	375	2	Q82QF4_STRAW	Q82qf4 streptomyce
87	35	70.0	377	2	O08468_STRHA	O08468 streptomyce
88	35	70.0	381	2	Q54331_STRLI	Q54331 streptomyce
89	35	70.0	381	2	Q9RJY3_STRCO	Q9rjy3 streptomyce
90	35	70.0	382	2	Q59963_STRRO	Q59963 streptomyce
91	35	70.0	383	2	Q67Y86_ARATH	Q67y86 arabidopsis
92	35	70.0	384	2	Q9X602_STRVD	Q9x602 streptomyce
93	35	70.0	390	2	Q7PML5_ANOGA	Q7pml5 anopheles g
94	35	70.0	390	2	Q5GWP9_XANOR	Q5gwp9 xanthomonas
95	35	70.0	401	2	Q45B43_9BURK	Q45b43 burkholderi
96	35	70.0	401	2	Q4LSJ5_9BURK	Q4lsj5 burkholderi
97	35	70.0	406	2	Q2NZV2_XANOR	Q2nzv2 xanthomonas
98	35	70.0	410	2	Q43NH3_SOLUS	Q43nh3 solibacter
99	35	70.0	439	2	Q4RS96_TETNG	Q4rs96 tetraodon n
100	35	70.0	450	1	CSK_CHICK	P41239 gallus gall

ALIGNMENTS

```
RESULT 1
Q3TLX4_MOUSE
ID   Q3TLX4_MOUSE   PRELIMINARY;   PRT;   368 AA.
AC   Q3TLX4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
DE   library, clone:G830026O06 product:lymphocyte protein tyrosine kinase,
DE   full insert sequence. (Fragment).
GN   Name=Lck;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK166263; BAE38668.1; -; mRNA.
DR   MGI; MGI:96756; Lck.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   368 AA;  42018 MW;  7AB6AE53AF1A5059 CRC64;

  Query Match             100.0%;  Score 50;  DB 2;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db         67 HYTNASDGL 75


RESULT 2
Q4FZR6_RAT
ID   Q4FZR6_RAT     PRELIMINARY;   PRT;   379 AA.
AC   Q4FZR6;
DT   30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   30-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Lck_mapped protein (Fragment).
GN   Name=Lck_mapped;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC099218; AAH99218.1; -; mRNA.
DR   SMR; Q4FZR6; 2-379.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   379 AA;  43336 MW;  7CDEB573BAFB53AB CRC64;

  Query Match             100.0%;  Score 50;  DB 2;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db         78 HYTNASDGL 86
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RESULT 3
LCK_AOTNA
ID   LCK_AOTNA      STANDARD;      PRT;   508 AA.
AC   Q5PXS1;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 3.
DT   07-MAR-2006, entry version 13.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Perez-Quintero L.A., Vernot J.P.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY821852; AAV70114.2; -; mRNA.
DR   SMR; Q5PXS1; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088123.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58041 MW;  8B61951BC192A3A4 CRC64;

  Query Match             100.0%;  Score 50;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        207 HYTNASDGL 215


RESULT 4
LCK_HUMAN
ID   LCK_HUMAN      STANDARD;      PRT;   508 AA.
AC   P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 5.
DT   07-MAR-2006, entry version 87.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-
DE   specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87133831; PubMed=3493153;
RA   Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
RA   Mak T.W.;
RT   "A human T cell-specific cDNA clone (YT16) encodes a protein with
RT   extensive homology to a family of protein-tyrosine kinases.";
```

RL Eur. J. Immunol. 16:1643-1646(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=89123626; PubMed=3265417;
RA Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
RA Wilson C.B.;
RT "Structure and expression of lck transcripts in human lymphoid
RT cells.";
RL J. Cell. Biochem. 38:117-126(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
RA Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
RA Benarous R.;
RT "Structure of the human lck gene: differences in genomic organisation
RT within src-related genes affect only N-terminal exons.";
RL Gene 84:105-113(1989).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;
RP VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.
RC TISSUE=Leukemia;
RX MEDLINE=94187714; PubMed=8139546;
RA Wright D.D., Sefton B.M., Kamps M.P.;
RT "Oncogenic activation of the Lck protein accompanies translocation of
RT the LCK gene in the human HSB2 T-cell leukemia.";
RL Mol. Cell. Biol. 14:2429-2437(1994).
RN [5]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.
RC TISSUE=Leukemic T-cell;
RX MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
RA Vogel L.B., Arthur R., Fujita D.J.;
RT "An aberrant lck mRNA in two human T-cell lines.";
RL Biochim. Biophys. Acta 1264:168-172(1995).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
RN [9]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89313764; PubMed=2787474;
RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA Miyamoto N.G., Mak T.W.;
RT "Structure of the two promoters of the human lck gene: differential
RT accumulation of two classes of lck transcripts in T cells.";
RL Mol. Cell. Biol. 9:2173-2180(1989).
RN [10]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.
RC TISSUE=Peripheral blood lymphocyte;
RX MEDLINE=20462621; PubMed=11009097;
RX DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
RA Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S.,
RA Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA Baldari C.T.;
RT "Defective recruitment and activation of ZAP-70 in common variable
RT immunodeficiency patients with T cell defects.";
RL Eur. J. Immunol. 30:2632-2638(2000).
RN [11]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 367-508.
RX MEDLINE=88217332; PubMed=2835736;
RA Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT and other non-lymphoid human tumor cell lines.";
RL Oncogene Res. 1:357-374(1987).
RN [12]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 374-508.
RX MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA Linna T.J.;
RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT p56LSTRA.";
RL Biochim. Biophys. Acta 888:286-295(1986).
RN [13]
RP PHOSPHORYLATION SITE TYR-504.
RX MEDLINE=92347326; PubMed=1639064;
RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA Amrein K.E., Autero M., Burn P., Alitalo K.;
RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT down regulates its catalytic activity.";
RL EMBO J. 11:2919-2924(1992).
RN [14]
RP INTERACTION WITH PI3K.
RX MEDLINE=94067101; PubMed=7504174;
RA Vogel L.B., Fujita D.J.;
RT "The SH3 domain of p56lck is involved in binding to
RT phosphatidylinositol 3'-kinase from T lymphocytes.";
RL Mol. Cell. Biol. 13:7408-7417(1993).
RN [15]
RP INTERACTION WITH KHDRBS1.
RX MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;
RA Vogel L.B., Fujita D.J.;
RT "p70 phosphorylation and binding to p56lck is an early event in
RT interleukin-2-induced onset of cell cycle progression in T-
RT lymphocytes.";
RL J. Biol. Chem. 270:2506-2511(1995).
RN [16]
RP INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.
RX PubMed=8618896;
RA Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;
RT "Phosphotyrosine-independent binding of a 62-kDa protein to the src
RT homology 2 (SH2) domain of p56lck and its regulation by
RT phosphorylation of Ser-59 in the lck unique N-terminal region.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).
RN [17]
RP INTERACTION WITH HIV-1 NEF.
RX MEDLINE=96386556; PubMed=8794306;
RA Greenway A.L., Azad A., Mills J., McPhee D.A.;
RT "Human immunodeficiency virus type 1 Nef binds directly to LCK and
RT mitogen-activated protein kinase, inhibiting kinase activity.";
RL J. Virol. 70:6701-6708(1996).
RN [18]
RP REVIEW.
RX PubMed=10848956;
RA Isakov N., Biesinger B.;
RT "Lck protein tyrosine kinase is a key regulator of T-cell activation
RT and a target for signal intervention by Herpesvirus saimiri and other

```
RT   viral gene products.";
RL   Eur. J. Biochem. 267:3413-3421(2000).
RN   [19]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [20]
RP   MASS SPECTROMETRY.
RC   TISSUE=Mammary cancer;
RX   MEDLINE=21829512; PubMed=11840567;
RX   DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
RA   Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA   Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA   Zvelebil M.J.;
RT   "Cluster analysis of an extensive human breast cancer cell line
RT   protein expression map database.";
RL   Proteomics 2:212-223(2002).
RN   [21]
RP   INTERACTION WITH LIME1.
RX   PubMed=14610046; DOI=10.1084/jem.20031484;
RA   Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
RA   Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
RA   Horejsi V.;
RT   "LIME: a new membrane raft-associated adaptor protein involved in CD4
RT   and CD8 coreceptor signaling.";
RL   J. Exp. Med. 198:1453-1462(2003).
RN   [22]
RP   INTERACTION WITH LIME1.

  Query Match             100.0%;  Score 50;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        207 HYTNASDGL 215


RESULT 5
LCK_MOUSE
ID   LCK_MOUSE      STANDARD;      PRT;   508 AA.
AC   P06240; Q61794; Q61795; Q62320; Q91X65;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   25-OCT-2005, sequence version 3.
DT   07-MAR-2006, entry version 74.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).
GN   Name=Lck; Synonyms=Lsk-t;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;
RA   Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;
RT   "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and
RT   overexpressed in the murine T cell lymphoma LSTRA.";
RL   Cell 43:393-404(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86146842; PubMed=3081813;
RA   Voronova A.F., Sefton B.M.;
RT   "Expression of a new tyrosine protein kinase is stimulated by
RT   retrovirus promoter insertion.";
RL   Nature 319:682-685(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89096891; PubMed=2850479;
RA   Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT   "Structure of the murine lck gene and its rearrangement in a murine
RT   lymphoma cell line.";
RL   Mol. Cell. Biol. 8:3058-3064(1988).
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RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.
RX   MEDLINE=88142832; PubMed=3501824;
RA   Voronova A.F., Adler H.T., Sefton B.M.;
RT   "Two lck transcripts containing different 5' untranslated regions are
RT   present in T cells.";
RL   Mol. Cell. Biol. 7:4407-4413(1987).
RN   [7]
RP   MUTAGENESIS OF TYR-504.
RX   MEDLINE=88248001; PubMed=3380790;
RA   Amrein K.E., Sefton B.M.;
RT   "Avian reovirus mRNAs are nonfunctional in infected mouse cells:
RT   translational basis for virus host-range restriction.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).
RN   [8]
RP   INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19
RP   AND CYS-22.
RX   MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;
RA   Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,
RA   Littman D.R.;
RT   "Interaction of the unique N-terminal region of tyrosine kinase p56lck
RT   with cytoplasmic domains of CD4 and CD8 is mediated by cysteine
RT   motifs.";
RL   Cell 60:755-765(1990).
RN   [9]
RP   MUTAGENESIS.
RX   MEDLINE=93059694; PubMed=1279202;
RA   Hurley T.R., Amrein K.E., Sefton B.M.;
RT   "Creation and characterization of temperature-sensitive mutants of the
RT   lck tyrosine protein kinase.";
RL   J. Virol. 66:7406-7413(1992).
RN   [10]
RP   MUTAGENESIS OF LYS-272.
RX   MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;
RA   Abraham N., Miceli M.C., Parnes J.C., Veillette A.;
RT   "Enhancement of T-cell responsiveness by the lymphocyte-specific
RT   tyrosine protein kinase p56lck.";
RL   Nature 350:62-66(1991).
RN   [11]
RP   MUTAGENESIS OF TYR-504.
RX   MEDLINE=91219495; PubMed=1708890;
RA   Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;
RT   "Thymic tumorigenesis induced by overexpression of p56lck.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
RN   [12]
RP   PHOSPHORYLATION BY CSK.
RX   PubMed=8371758; DOI=10.1038/365156a0;
RA   Chow L.M., Fournel M., Davidson D., Veillette A.;
RT   "Negative regulation of T-cell receptor signalling by tyrosine protein
RT   kinase p50csk.";
RL   Nature 365:156-160(1993).
RN   [13]
RP   MUTAGENESIS.
RX   MEDLINE=93133805; PubMed=8421674;
RA   Carrera A.C., Alexandrov K., Roberts T.M.;
RT   "The conserved lysine of the catalytic domain of protein kinases is
RT   actively involved in the phosphotransfer reaction and not required for
RT   anchoring ATP.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
RN   [14]
RP   PALMITOYLATION.
RX   MEDLINE=94019312; PubMed=8413237;
RA   Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
RT   "Palmitylation of an amino-terminal cysteine motif of protein tyrosine
RT   kinases p56lck and p59fyn mediates interaction with glycosyl-
RT   phosphatidylinositol-anchored proteins.";
RL   Mol. Cell. Biol. 13:6385-6392(1993).
RN   [15]
RP   PALMITOYLATION.
RX   MEDLINE=95071286; PubMed=7980442;
RA   Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;
RT   "Palmitoylation of multiple Src-family kinases at a homologous N-
RT   terminal motif.";
RL   Biochem. J. 303:749-753(1994).
RN   [16]
RP   INTERACTION WITH CBLB.
RX   PubMed=10646608; DOI=10.1038/35003228;
RA   Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,
RA   Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,
RA   Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,
RA   Penninger J.M.;
RT   "Negative regulation of lymphocyte activation and autoimmunity by the
RT   molecular adaptor Cbl-b.";
RL   Nature 403:211-216(2000).
RN   [17]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [18]
RP   PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.
RX   PubMed=15592455; DOI=10.1038/nbt1046;
RA   Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA   Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT   "Immunoaffinity profiling of tyrosine phosphorylation in cancer

  Query Match             100.0%;  Score 50;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        207 HYTNASDGL 215


RESULT 6
LCK_SAISC
ID   LCK_SAISC      STANDARD;      PRT;   508 AA.
AC   Q95KR7;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 2.
DT   07-MAR-2006, entry version 26.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], ENZYME REGULATION, AND INTERACTION WITH
RP   SAIMIRINE HERPESVIRUS 2 TIP.
RC   TISSUE=T-cell;
RX   MEDLINE=21424508; PubMed=11533187;
RX   DOI=10.1128/JVI.75.19.9252-9261.2001;
RA   Greve T., Tamgueney G., Fleischer B., Fickenscher H., Broeker B.M.;
RT   "Downregulation of p56Lck tyrosine kinase activity in T cells of
RT   squirrel monkeys (Saimiri sciureus) correlates with the non-
RT   transforming and apathogenic properties of herpesvirus saimiri in its
RT   natural host.";
RL   J. Virol. 75:9252-9261(2001).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
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CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- ENZYME REGULATION: Regulated by phosphatases.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity). Interacts with saimirine herpesvirus 2 TIP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed specificaly in lymphoid cells.
CC   -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout
CC       T-cell ontogeny.
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This
CC       phosphorylation downregulates catalytic activity. Phosphorylated
CC       on Tyr-393 either by itself or another kinase, leading to
CC       increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   -!- CAUTION: LCK seems to be active in all vertebrates, except in
CC       squirrel monkey T-cells, in which it is inactivated. The reason
CC       seems to be that squirrel monkey are the natural host for
CC       Saimiriine herpesvirus 2, which is able to efficiently transform
CC       T-cells through a mecanism involving viral Tip/ host LCK
CC       interaction. Its inactivation may a mecanism that specificaly
CC       counteracts the transformation effects of viral Tip.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277921; CAC38871.1; -; mRNA.
DR   HSSP; P06239; 1LKK.
DR   SMR; Q95KR7; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088127.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58122 MW;  5088C64061853819 CRC64;

  Query Match             100.0%;  Score 50;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        207 HYTNASDGL 215


RESULT 7
Q7RTZ3_HUMAN
ID   Q7RTZ3_HUMAN   PRELIMINARY;   PRT;   509 AA.
AC   Q7RTZ3;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Protein tyrosine kinase.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22289034; PubMed=12401726;
RA   Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,
RA   Naquet P., Matsuda F., Imbert J., Vialettes B.;
RT   "No association between lck gene polymorphisms and protein level in
RT   type 1 diabetes.";
RL   Diabetes 51:3326-3330(2002).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BN000073; CAD55807.1; -; Genomic_DNA.
DR   HSSP; P06239; 1BHF.
DR   SMR; Q7RTZ3; 65-509.
DR   Ensembl; ENSG00000182866; Homo sapiens.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
```

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DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   509 AA;  58001 MW;  44BFF0D43FFB420D CRC64;

  Query Match             100.0%;  Score 50;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        208 HYTNASDGL 216


RESULT 8
Q95M32_9PRIM
ID   Q95M32_9PRIM   PRELIMINARY;   PRT;   509 AA.
AC   Q95M32;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Lck protein.
GN   Name=lck;
OS   Hylobates sp. (gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Hylobatidae; Hylobates.
OX   NCBI_TaxID=9581;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
RA   Picard C., Greenway A., Holloway G., Olive D., Collette Y.;
RT   "Interaction with simian Hck tyrosine kinase reveals convergent
RT   evolution of the Nef protein from simian and human immunodeficiency
RT   viruses despite differential molecular surface usage.";
RL   Virology 295:320-327(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Picard C.;
RL   Thesis (2001), Department of Experimental Oncology laboratory, U.
CC   ----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
DR   EMBL; AJ320182; CAC44027.1; -; mRNA.
DR   HSSP; P06239; 1LCK.
DR   SMR; Q95M32; 65-509.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   509 AA;  57947 MW;  F1BFE5C237C8DB7E CRC64;

  Query Match             100.0%;  Score 50;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||||||||
Db        208 HYTNASDGL 216


RESULT 9
O73786_XENLA
ID   O73786_XENLA   PRELIMINARY;   PRT;   450 AA.
AC   O73786;
DT   01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT   01-AUG-1998, sequence version 1.
DT   07-FEB-2006, entry version 27.
DE   C-Src kinase.
GN   Name=CSK;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
```

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OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Murphy S.M., Morgan D.O.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF052430; AAC05835.1; -; mRNA.
DR   HSSP; P41240; 1BYG.
DR   SMR; O73786; 4-449.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   450 AA;  50807 MW;  F02FE0557679BA53 CRC64;

  Query Match             82.0%;  Score 41;  DB 2;  Length 450;
  Best Local Similarity   77.8%;  Pred. No. 15;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||| :|||
Db        155 HYTNDADGL 163


RESULT 10
Q81295_9HEPC
ID   Q81295_9HEPC   PRELIMINARY;   PRT;   193 AA.
AC   Q81295;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-FEB-2005, sequence version 3.
DT   07-FEB-2006, entry version 23.
DE   Core protein/E1 protein (Fragment).
OS   Hepatitis C virus genotype 4.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC   Hepacivirus.
OX   NCBI_TaxID=33745;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CAR4/1205;
RA   Stuyver L., Fretz C., Jeannel D.;
RT   "Hepatitis C virus infection in a rural population in Central African
RT   Republic.";
RL   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L36439; AAA45537.1; -; Genomic_RNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR002521; HCV_core.
DR   InterPro; IPR002519; HCV_env.
DR   Pfam; PF01542; HCV_core; 1.
DR   Pfam; PF01539; HCV_env; 1.
KW   Envelope protein; Transmembrane.
FT   CHAIN        <1     65       core protein.
FT   CHAIN        66   >193       E1 protein.
FT   NON_TER       1      1
FT   NON_TER     193    193
SQ   SEQUENCE   193 AA;  20366 MW;  2E167CE47CEC828F CRC64;

  Query Match             80.0%;  Score 40;  DB 2;  Length 193;
  Best Local Similarity   87.5%;  Pred. No. 9.2;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 HYTNASDG 8
              || |||||
Db         67 HYRNASDG 74


RESULT 11
Q4R6L8_MACFA
ID   Q4R6L8_MACFA   PRELIMINARY;   PRT;   408 AA.
AC   Q4R6L8;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Testis cDNA, clone: QtsA-17706, similar to human fyn-related kinase
DE   (FRK),.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15944441; DOI=10.1093/molbev/msi187;
RA   Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA   Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT   "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT   Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RL   Mol. Biol. Evol. 22:1976-1982(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   International consortium for macaque cDNA sequencing and analysis;
RT   "DNA sequences of macaque genes expressed in brain or testis and its
RT   evolutionary implications.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB169165; BAE01257.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
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DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   Kinase.
SQ   SEQUENCE   408 AA;  47153 MW;  1AFE91AC88554555 CRC64;

  Query Match             80.0%;  Score 40;  DB 2;  Length 408;
  Best Local Similarity   77.8%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||  ||||
Db         95 HYTKTSDGL 103


RESULT 12
FRK_HUMAN
ID   FRK_HUMAN      STANDARD;      PRT;   505 AA.
AC   P42685; Q13128;
DT   01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1995, sequence version 1.
DT   07-MAR-2006, entry version 55.
DE   Tyrosine-protein kinase FRK (EC 2.7.1.112) (Nuclear tyrosine protein
DE   kinase RAK).
GN   Name=FRK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Lymphoid;
RX   MEDLINE=94171047; PubMed=7510261; DOI=10.1016/0378-1119(94)90817-6;
RA   Lee J., Wang Z., Luoh S.-M., Wood W.I., Scadden D.T.;
RT   "Cloning of FRK, a novel human intracellular SRC-like tyrosine kinase-
RT   encoding gene.";
RL   Gene 138:247-251(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=95210168; PubMed=7696183;
RA   Cance W.G., Craven R.J., Bergman M., Xu L.H., Alitalo K., Liu E.T.;
RT   "Rak, a novel nuclear tyrosine kinase expressed in epithelial cells.";
RL   Cell Growth Differ. 5:1347-1355(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Urinary bladder;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   PARTIAL NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93293373; PubMed=8099900;
RA   Cance W.G., Craven R.J., Weiner T.M., Liu E.T.;
RT   "Novel protein kinases expressed in human breast cancer.";
RL   Int. J. Cancer 54:571-577(1993).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (Probable).
CC   -!- TISSUE SPECIFICITY: Restricted to cells lines derived from tissues
CC       of lymphoid, brain, breast, colon and bladder origin.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
DR   EMBL; U00803; AAA18284.1; -; mRNA.
DR   EMBL; U22322; AAC50116.1; -; mRNA.
DR   EMBL; BC012916; AAH12916.1; -; mRNA.
DR   PIR; I38396; I38396.
DR   HSSP; P00523; 2PTK.
DR   Ensembl; ENSG00000111816; Homo sapiens.
DR   H-InvDB; HIX0006158; -.
DR   HGNC; HGNC:3955; FRK.
DR   MIM; 606573; gene.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0004715; F:non-membrane spanning protein tyrosine kina. . .; TAS.
DR   GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Polymorphism; SH2 domain; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   CHAIN         1    505       Tyrosine-protein kinase FRK.
FT                                /FTId=PRO_0000088097.
FT   DOMAIN       42    110       SH3.
FT   DOMAIN      116    208       SH2.
FT   DOMAIN      234    491       Protein kinase.
FT   NP_BIND     240    248       ATP (By similarity).
FT   ACT_SITE    354    354       Proton acceptor (By similarity).
FT   BINDING     262    262       ATP (By similarity).
FT   MOD_RES     387    387       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   VARIANT     122    122       G -> R (in dbSNP:3756772).
FT                                /FTId=VAR_006283.
FT   CONFLICT    115    115       P -> A (in Ref. 2).
SQ   SEQUENCE   505 AA;  58254 MW;  06EC050DDBCD930B CRC64;

  Query Match             80.0%;  Score 40;  DB 1;  Length 505;
  Best Local Similarity   77.8%;  Pred. No. 28;
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  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||  ||||
Db        192 HYTKTSDGL 200


RESULT 13
Q9NTR5_HUMAN
ID   Q9NTR5_HUMAN   PRELIMINARY;   PRT;   505 AA.
AC   Q9NTR5;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   04-JAN-2005, sequence version 2.
DT   07-FEB-2006, entry version 22.
DE   Fyn-related kinase.
GN   Name=FRK; ORFNames=RP11-702N8.1-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Williams S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Lloyd C.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AL121963; CAB87592.2; -; Genomic_DNA.
DR   EMBL; AL357141; CAB87592.2; JOINED; Genomic_DNA.
DR   EMBL; AL357141; CAI16469.1; -; Genomic_DNA.
DR   EMBL; AL121963; CAI16469.1; JOINED; Genomic_DNA.
DR   Ensembl; ENSG00000111816; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   505 AA;  58254 MW;  06EC050DDBCD930B CRC64;

  Query Match             80.0%;  Score 40;  DB 2;  Length 505;
  Best Local Similarity   77.8%;  Pred. No. 28;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||  ||||
Db        192 HYTKTSDGL 200


RESULT 14
Q3ZCM0_BOVIN
ID   Q3ZCM0_BOVIN   PRELIMINARY;   PRT;   509 AA.
AC   Q3ZCM0;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein MGC126900.
GN   Name=MGC126900;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC102046; AAI02047.1; -; mRNA.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
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DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   509 AA;  58116 MW;  CE0E80DCD6D0F2F8 CRC64;

  Query Match             80.0%;  Score 40;  DB 2;  Length 509;
  Best Local Similarity   77.8%;  Pred. No. 29;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              || | ||||
Db        208 HYMNTSDGL 216


RESULT 15
Q9SH39_ARATH
ID   Q9SH39_ARATH   PRELIMINARY;   PRT;   323 AA.
AC   Q9SH39;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   F2K11.9.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA   Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA   Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA   Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA   Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA   Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA   Ecker J.R.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA   Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,
RA   Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA   Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
RA   Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA   Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
RA   Ecker J.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA   Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA   Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA   Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA   Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA   Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA   Theologis A., Ecker J.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AC008047; AAF19714.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004550; F:nucleoside diphosphate kinase activity; IEA.
DR   GO; GO:0006241; P:CTP biosynthesis; IEA.
DR   GO; GO:0006183; P:GTP biosynthesis; IEA.
DR   GO; GO:0006228; P:UTP biosynthesis; IEA.
DR   InterPro; IPR002902; DUF26.
DR   InterPro; IPR001564; NDK.
DR   Pfam; PF01657; DUF26; 2.
SQ   SEQUENCE   323 AA;  35717 MW;  1FB68B95F78ECCE4 CRC64;

  Query Match             78.0%;  Score 39;  DB 2;  Length 323;
  Best Local Similarity   66.7%;  Pred. No. 27;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              ||:||::||
Db         67 HYSNATEGL 75


RESULT 16
Q5Q0E2_ARATH
ID   Q5Q0E2_ARATH   PRELIMINARY;   PRT;   324 AA.
AC   Q5Q0E2;
DT   04-JAN-2005, integrated into UniProtKB/TrEMBL.
DT   04-JAN-2005, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Hypothetical protein.
GN   ORFNames=AT1G63550, At1g63550;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Xiao Y., Underwood B., Moskal W., Wang W., Redman J., Wu H.C.,
RA   Utterback T., Town C.D.;
RT   "Reconstruction of cDNA sequences for hypothetical genes in
RT   Arabidopsis thaliana from 5' and 3' RACE products.";
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Underwood B.A., Xiao Y., Moskal W., Monaghan E., Wang W., Redman J.,
RA   Wu H.C., Utterback T., Town C.D.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY800609; AAV68845.1; -; mRNA.
DR   EMBL; AY954768; AAX55094.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004550; F:nucleoside diphosphate kinase activity; IEA.
DR   GO; GO:0006241; P:CTP biosynthesis; IEA.
DR   GO; GO:0006183; P:GTP biosynthesis; IEA.
DR   GO; GO:0006228; P:UTP biosynthesis; IEA.
DR   InterPro; IPR002902; DUF26.
DR   InterPro; IPR001564; NDK.
DR   Pfam; PF01657; DUF26; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   324 AA;  35754 MW;  A389AA8030E1D89F CRC64;

  Query Match             78.0%;  Score 39;  DB 2;  Length 324;
  Best Local Similarity   66.7%;  Pred. No. 27;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              ||:||::||
Db         67 HYSNATEGL 75


RESULT 17
Q38KH2_BOVIN
ID   Q38KH2_BOVIN   PRELIMINARY;   PRT;   276 AA.
AC   Q38KH2;
DT   22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT   22-NOV-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Truncated HCK tyrosine kinase.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
```

```
RP   NUCLEOTIDE SEQUENCE.
RA   Lalancette C., Bordeleau L.-J., Faure R.L., Leclerc P.;
RT   "Bull Testicular Haploid Germ Cells Express a Messenger Encoding for a
RT   Truncated Form of the Protein Tyrosine Kinase HCK.";
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; DQ219802; ABB03777.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
KW   Kinase.
SQ   SEQUENCE   276 AA;  31529 MW;  A3CBD992B78E2CBB CRC64;

  Query Match             76.0%;  Score 38;  DB 2;  Length 276;
  Best Local Similarity   77.8%;  Pred. No. 37;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              ||  |||||
Db        122 HYKKASDGL 130


RESULT 18
Q8AWF1_BRARE
ID   Q8AWF1_BRARE   PRELIMINARY;   PRT;   525 AA.
AC   Q8AWF1;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   Yes-relayed kinase.
GN   Name=yrk;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Mead R.S., Horsfeild J.A., Khan L.B., Postlethwait J.H., Crosier K.E.,
RA   Crosier P.S.;
RT   "Zebrafish yrk is a Src-family kinase implicated in embryonic vascular
RT   development.";
RL   Genome Res. 0:0-0(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY169369; AAN87886.1; -; mRNA.
DR   HSSP; P00523; 2PTK.
DR   SMR; Q8AWF1; 1-130, 76-525.
DR   Ensembl; ENSDARG00000004378; Danio rerio.
DR   ZFIN; ZDB-GENE-030131-9517; yrk.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   525 AA;  59156 MW;  4A22FF15FC9C684B CRC64;

  Query Match             76.0%;  Score 38;  DB 2;  Length 525;
  Best Local Similarity   66.7%;  Pred. No. 78;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              ||| ::|||
Db        221 HYTGSNDGL 229


RESULT 19
Q7QE10_ANOGA
ID   Q7QE10_ANOGA   PRELIMINARY;   PRT;   943 AA.
AC   Q7QE10;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 2.
DT   07-FEB-2006, entry version 19.
DE   ENSANGP00000000570 (Fragment).
GN   ORFNames=ENSANGG00000000517;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
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CC   ---------------------------------------------------------------------
DR   EMBL; AAAB01008848; EAA07075.2; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00023; Ank; 5.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 2.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
```

```
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 2.
DR   SMART; SM00248; ANK; 3.
DR   SMART; SM00252; SH2; 2.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 3.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 2.
KW   ANK repeat; Tyrosine-protein kinase.
FT   NON_TER     943     943
SQ   SEQUENCE   943 AA;  105680 MW;  E0FA0F3F24FFDA1C CRC64;

  Query Match             76.0%;  Score 38;  DB 2;  Length 943;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HYTNASDGL 9
              |||  |||| 
Db        391 HYTRFSDGL 399


RESULT 20
Q2PBR5_9VIRU
ID   Q2PBR5_9VIRU   PRELIMINARY;   PRT;  1114 AA.
AC   Q2PBR5;
DT   07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   07-FEB-2006, sequence version 1.
DT   07-FEB-2006, entry version 1.
DE   Polyprotein.
OS   Tellina virus 1.
OC   Viruses; unclassified viruses.
OX   NCBI_TaxID=321302;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Nobiron I., Galloux M., Henry C., Huet J.C.;
RT   "Genome structure and polypeptides characterization of Tellina virus
RT   1.";
RL   Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Delmas B.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ920335; CAI74981.1; -; Genomic_RNA.
KW   Polyprotein.
FT   CHAIN         2    451       VP2 protein.
FT   CHAIN       452    492       pep41 protein.
FT   CHAIN       493    499       pep7 protein.
FT   CHAIN       500    512       pep13 protein.
FT   CHAIN       513    618       X protein.
FT   CHAIN       619    830       VP4 protein.
FT   CHAIN       831   1114       VP3 protein.
SQ   SEQUENCE   1114 AA;  119739 MW;  658BB0EEDF059E42 CRC64;

  Query Match             76.0%;  Score 38;  DB 2;  Length 1114;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 HYTNASDG 8
              ||| |||| 
Db         72 HYTYASDG 79


RESULT 21
Q6IJB6_DROME
ID   Q6IJB6_DROME   PRELIMINARY;   PRT;   351 AA.
AC   Q6IJB6;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   HDC15303.
GN   ORFNames=HDC15303;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
RA   Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,
RA   Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
RA   Paro R.;
RT   "An integrated gene annotation and transcriptional profiling approach
RT   towards the full gene content of the Drosophila genome.";
RL   Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BK002800; DAA04305.1; -; Genomic_DNA.
DR   InterPro; IPR000194; ATPase_a/bcentre.
DR   PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
SQ   SEQUENCE   351 AA;  36653 MW;  588437B6067094C4 CRC64;

  Query Match             74.0%;  Score 37;  DB 2;  Length 351;
  Best Local Similarity   75.0%;  Pred. No. 79;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HYTNASDG 8
              || || || 
Db        280 HYNNAKDG 287


RESULT 22
Q6W9M4_PENMA
ID   Q6W9M4_PENMA   PRELIMINARY;   PRT;   358 AA.
AC   Q6W9M4;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   G-alpha subunit.
GN   Name=gasB;
OS   Penicillium marneffei.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=37727;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Zuber S., Hynes M.J., Andrianopoulos A.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY301989; AAQ24336.1; -; Genomic_DNA.
DR   HSSP; P04896; 1AZS.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR002975; Fungi_GproteinA.
DR   InterPro; IPR001019; Gprotein_alph_bd.
DR   InterPro; IPR011025; GproteinA_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR01241; GPROTEINAFNG.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
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SQ   SEQUENCE   358 AA;  41206 MW;  060309D95BAFF6C8 CRC64;

  Query Match             74.0%;  Score 37;  DB 2;  Length 358;
  Best Local Similarity   85.7%;  Pred. No. 80;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASD 7
              |||||:|
Db        327 HYTNATD 333


RESULT 23
Q5DPY8_PARBR
ID   Q5DPY8_PARBR   PRELIMINARY;   PRT;   359 AA.
AC   Q5DPY8;
DT   29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT   29-MAR-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Small G-protein GPA2.
GN   Name=gpa2;
OS   Paracoccidioides brasiliensis.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Onygenales; mitosporic Onygenales; Paracoccidioides.
OX   NCBI_TaxID=121759;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Chen D., Borges-Walmsley M.I., Walmsley A.R.;
RT   "Paracoccidioides brasiliensis GPA2.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY550248; AAT40564.1; -; Genomic_DNA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR002975; Fungi_GproteinA.
DR   InterPro; IPR001019; Gprotein_alph_bd.
DR   InterPro; IPR011025; GproteinA_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR01241; GPROTEINAFNG.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   359 AA;  41158 MW;  EA861CD0FAE976AB CRC64;

  Query Match             74.0%;  Score 37;  DB 2;  Length 359;
  Best Local Similarity   85.7%;  Pred. No. 81;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASD 7
              |||||:|
Db        328 HYTNATD 334


RESULT 24
Q2URQ7_ASPOR
ID   Q2URQ7_ASPOR   PRELIMINARY;   PRT;   359 AA.
AC   Q2URQ7;
DT   24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT   24-JAN-2006, sequence version 1.
DT   07-MAR-2006, entry version 3.
DE   G-protein alpha subunit.
GN   ORFNames=AO090005000727;
OS   Aspergillus oryzae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5062;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=RIB 40;
RX   PubMed=16372010; DOI=10.1038/nature04300;
RA   Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
RA   Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
RA   Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA   Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
RA   Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,
RA   Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,
RA   Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA   Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA   Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA   Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
RA   Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
RA   Kuhara S., Ogasawara N., Kikuchi H.;
RT   "Genome sequencing and analysis of Aspergillus oryzae.";
RL   Nature 438:1157-1161(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; AP007151; BAE55758.1; -; Genomic_DNA.
SQ   SEQUENCE   359 AA;  41202 MW;  70EEC45051B2243A CRC64;

  Query Match             74.0%;  Score 37;  DB 2;  Length 359;
  Best Local Similarity   85.7%;  Pred. No. 81;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASD 7
              |||||:|
Db        328 HYTNATD 334


RESULT 25
Q4WYB0_ASPFU
ID   Q4WYB0_ASPFU   PRELIMINARY;   PRT;   359 AA.
AC   Q4WYB0;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   G protein complex alpha subunit (GanA), putative.
GN   ORFNames=Afu3g12400;
OS   Aspergillus fumigatus (Sartorya fumigata).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5085;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Af293 / CBS 101355 / FGSC A1100;
RX   PubMed=16372009; DOI=10.1038/nature04332;
RA   Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
RA   Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
RA   Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
RA   Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
RA   Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA   Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
RA   Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,
RA   Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
RA   Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A.,
RA   Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
RA   Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,
RA   Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA   Rabbinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
RA   Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA   Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA   Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA   Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA   White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,
RA   Machida M., Hall N., Barrell B.G., Denning D.W.;
RT   "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT   Aspergillus fumigatus.";
RL   Nature 438:1151-1156(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ----------------------------------------------------------------------
DR   EMBL; AAHF01000002; EAL92343.1; -; Genomic_DNA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR002975; Fungi_GproteinA.
DR   InterPro; IPR001019; Gprotein_alph_bd.
DR   InterPro; IPR011025; GproteinA_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR01241; GPROTEINAFNG.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
KW   Complete proteome.
SQ   SEQUENCE   359 AA;  41397 MW;  CA1307C3019E1204 CRC64;

  Query Match             74.0%;  Score 37;  DB 2;  Length 359;
  Best Local Similarity   85.7%;  Pred. No. 81;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASD 7
              |||||:|
Db        328 HYTNATD 334


RESULT 26
Q60Q64_CAEBR
ID   Q60Q64_CAEBR   PRELIMINARY;   PRT;   360 AA.
AC   Q60Q64;
DT   23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT   23-NOV-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Hypothetical protein CBG21947 (Fragment).
GN   Name=CBG21947;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=AF16;
RX   PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA   Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N.,
RA   Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA   D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA   Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA   Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P.,
RA   Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M.,
RA   Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,
RA   Waterston R.H.;
RT   "The genome sequence of Caenorhabditis briggsae: a platform for
RT   comparative genomics.";
RL   PLoS Biol. 1:166-192(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ----------------------------------------------------------------------
DR   EMBL; CAAC01000127; CAE74258.1; -; Genomic_DNA.
DR   GO; GO:0019001; F:guanyl nucleotide binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001019; Gprotein_alph_bd.
DR   InterPro; IPR011025; GproteinA_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
KW   Complete proteome; Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   360 AA;  42040 MW;  890E3AD2E71AFC35 CRC64;

  Query Match             74.0%;  Score 37;  DB 2;  Length 360;
  Best Local Similarity   85.7%;  Pred. No. 81;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASD 7
              |||||:|
Db        328 HYTNATD 334


RESULT 27
Q9Y7E3_EMENI
ID   Q9Y7E3_EMENI   PRELIMINARY;   PRT;   361 AA.
AC   Q9Y7E3;
DT   01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1999, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   G protein alpha subunit homolog GanAp.
GN   Name=ganA;
OS   Emericella nidulans (Aspergillus nidulans).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=162425;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FGSC4;
RA   Chang M.H., Jahng K.-Y.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF142058; AAD34893.1; -; Genomic_DNA.
DR   HSSP; P04896; 1CUL.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR002975; Fungi_GproteinA.
DR   InterPro; IPR001019; Gprotein_alph_bd.
DR   InterPro; IPR011025; GproteinA_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR01241; GPROTEINAFNG.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
SQ   SEQUENCE   361 AA;  41576 MW;  EB22054B74D6F1AB CRC64;

  Query Match             74.0%;  Score 37;  DB 2;  Length 361;
  Best Local Similarity   85.7%;  Pred. No. 81;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASD 7
              |||||:|
Db        330 HYTNATD 336


RESULT 28
Q5B8P0_EMENI
ID   Q5B8P0_EMENI   PRELIMINARY;   PRT;   361 AA.
AC   Q5B8P0;
DT   26-APR-2005, integrated into UniProtKB/TrEMBL.
DT   26-APR-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein.
GN   ORFNames=AN3090.2;
OS   Aspergillus nidulans FGSC A4.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=227321;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=FGSC 4;
RX   PubMed=16372000; DOI=10.1038/nature04341;
RA   Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
RA   Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
RA   Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,
RA   Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C.,
RA   Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
RA   Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,
RA   Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
RA   Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
RA   Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,
RA   Sachs M.S., Osmani S.A., Birren B.W.;
RT   "Sequencing of Aspergillus nidulans and comparative analysis with A.
RT   fumigatus and A. oryzae.";
RL   Nature 438:1105-1115(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ---------------------------------------------------------------------
DR   EMBL; AACD01000051; EAA63661.1; -; Genomic_DNA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR002975; Fungi_GproteinA.
DR   InterPro; IPR001019; Gprotein_alph_bd.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   PRINTS; PR01241; GPROTEINAFNG.
DR   SMART; SM00275; G_alpha; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   361 AA;  41591 MW;  EB2EF55674D6F1B6 CRC64;

  Query Match            74.0%;  Score 37;  DB 2;  Length 361;
  Best Local Similarity  85.7%;  Pred. No. 81;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASD 7
              |||||:|
Db        330 HYTNATD 336


RESULT 29
Q4VT41_CAEBR
ID   Q4VT41_CAEBR   PRELIMINARY;   PRT;   368 AA.
AC   Q4VT41;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Gpa-11 (Fragment).
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AF16;
RA   Jovelin R., Phillips P.C.;
RT   "Functional constraint and divergence in the G protein family in
RT   Caenorhabditis elegans and Caenorhabditis briggsae.";
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY634289; AAW02895.1; -; Genomic_DNA.
DR   GO; GO:0019001; F:guanyl nucleotide binding; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001019; Gprotein_alph_bd.
DR   InterPro; IPR011025; GproteinA_insert.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   ProDom; PD000281; Gprotein_alpha; 1.
DR   SMART; SM00275; G_alpha; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   368 AA;  42833 MW;  4E7F153EF5B8DFF5 CRC64;

  Query Match            74.0%;  Score 37;  DB 2;  Length 368;
  Best Local Similarity  85.7%;  Pred. No. 83;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HYTNASD 7
              |||||:|
Db        336 HYTNATD 342


RESULT 30
Q4URA6_XANC8
ID   Q4URA6_XANC8   PRELIMINARY;   PRT;   405 AA.
AC   Q4URA6;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Xylanase.
GN   OrderedLocusNames=XC_3373;
OS   Xanthomonas campestris pv. campestris (strain 8004).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC   Xanthomonadaceae; Xanthomonas.
OX   NCBI_TaxID=314565;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15899963; DOI=10.1101/gr.3378705;
RA   Qian W., Jia Y., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F., Sun Q.,
RA   Ying G., Tang D.-J., Tang H., Wu W., Hao P., Wang L., Jiang B.-L.,
RA   Zeng S., Gu W.-Y., Lu G., Rong L., Tian Y., Yao Z., Fu G., Chen B.,
RA   Fang R., Qiang B., Chen Z., Zhao G.-P., Tang J.-L., He C.;
RT   "Comparative and functional genomic analyses of the pathogenicity of
RT   phytopathogen Xanthomonas campestris pv. campestris.";
RL   Genome Res. 15:757-767(2005).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; CP000050; AAY50417.1; -; Genomic_DNA.
DR   GO; GO:0005764; C:lysosome; IEA.
DR   GO; GO:0004348; F:glucosylceramidase activity; IEA.
DR   GO; GO:0007040; P:lysosome organization and biogenesis; IEA.
DR   GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR   GO; GO:0045493; P:xylan catabolism; IEA.
DR   InterPro; IPR001139; Glyco_hydro_30.
DR   PANTHER; PTHR11069; Glyco_hydro_30; 1.
DR   Pfam; PF02055; Glyco_hydro_30; 1.
KW   Complete proteome; Xylan degradation.
SQ   SEQUENCE   405 AA;  43309 MW;  3B22DE622C890CA0 CRC64;

  Query Match            74.0%;  Score 37;  DB 2;  Length 405;
  Best Local Similarity  75.0%;  Pred. No. 93;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 HYTNASDG 8
              |||: |||
Db        248 HYTDTSDG 255


Search completed: June 29, 2006, 09:29:46
Job time : 109.942 secs
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